

OM protein - protein search, using sw model

Run on: January 30, 2006, 09:06:47 ; Search time 161 Seconds

(without alignments)
39.439 Million cell updates/sec

Title: US-10-608-147-29

Perfect score: 53

Sequence: 1 IETWILRHP 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	120	2	Q67424_9FLAV
2	53	100.0	166	2	Q66346_9FLAV
3	53	100.0	280	2	Q80264_9FLAV
4	53	100.0	280	2	Q80265_9FLAV
5	53	100.0	280	2	Q80266_9FLAV
6	53	100.0	280	2	Q80267_9FLAV
7	53	100.0	555	1	POLG_DEN2H
8	53	100.0	578	2	012290_9FLAV
9	53	100.0	661	2	Q54186_9FLAV
10	53	100.0	661	2	Q5V187_9FLAV
11	53	100.0	661	2	Q5V188_9FLAV
12	53	100.0	661	2	Q5V189_9FLAV
13	53	100.0	661	2	Q5V190_9FLAV
14	53	100.0	661	2	Q5V191_9FLAV
15	53	100.0	661	2	Q5V192_9FLAV

16	53	100.0	661	2	Q5V193_9FLAV	Q5V193 dengue v1ru
17	53	100.0	661	2	Q5V194_9FLAV	Q5V194 dengue v1ru
18	53	100.0	661	2	Q5V195_9FLAV	Q5V195 dengue v1ru
19	53	100.0	661	2	Q5V196_9FLAV	Q5V196 dengue v1ru
20	53	100.0	716	2	Q6DUV2_9FLAV	Q6DUV2 dengue v1ru
21	53	100.0	724	2	Q51CU9_9FLAV	Q51CU9 dengue v1ru
22	53	100.0	745	2	Q6KEK9_9FLAV	Q6KEK9 dengue v1ru
23	53	100.0	757	2	Q5S8P1_9FLAV	Q5S8P1 dengue v1ru
24	53	100.0	757	2	Q5S8P2_9FLAV	Q5S8P2 dengue v1ru
25	53	100.0	757	2	Q6DUD9_9FLAV	Q6DUD9 dengue v1ru
26	53	100.0	763	2	Q51CU8_9FLAV	Q51CU8 dengue v1ru
27	53	100.0	775	2	Q66398_9FLAV	Q66398 dengue v1ru
28	53	100.0	775	2	Q8QY62_9FLAV	Q8QY62 dengue v1ru
29	53	100.0	775	2	Q8QY63_9FLAV	Q8QY63 dengue v1ru
30	53	100.0	775	2	Q8QY67_9FLAV	Q8QY67 dengue v1ru
31	53	100.0	779	2	Q88636_9FLAV	Q88636 dengue v1ru
32	53	100.0	1127	2	P87638_9FLAV	P87638 dengue v1ru
33	53	100.0	1127	2	P89531_9FLAV	P89531 dengue v1ru
34	53	100.0	1127	2	P89532_9FLAV	P89532 dengue v1ru
35	53	100.0	1127	2	Q66454_9FLAV	Q66454 dengue v1ru
36	53	100.0	1127	2	Q66455_9FLAV	Q66455 dengue v1ru
37	53	100.0	1127	2	Q66456_9FLAV	Q66456 dengue v1ru
38	53	100.0	1127	2	Q66457_9FLAV	Q66457 dengue v1ru
39	53	100.0	3388	1	POLG_DEN2P	P12823 d genome po
40	53	100.0	3391	1	POLG_DEN26	P29990 d genome po
41	53	100.0	3391	1	POLG_DEN27	P29991 d genome po
42	53	100.0	3391	1	POLG_DEN2J	P07564 d genome po
43	53	100.0	3391	1	POLG_DEN2N	P14340 d genome po
44	53	100.0	3391	2	009234_DEN26	009234 dengue v1ru
45	53	100.0	3391	2	011875_9FLAV	011875 dengue v1ru
46	53	100.0	3391	2	092752_9FLAV	092752 dengue v1ru
47	53	100.0	3391	2	092753_9FLAV	092753 dengue v1ru
48	53	100.0	3391	2	092754_9FLAV	092754 dengue v1ru
49	53	100.0	3391	2	092835_9FLAV	092835 dengue v1ru
50	53	100.0	3391	2	Q58Y66_9FLAV	Q58Y66 dengue v1ru
51	53	100.0	3391	2	Q58Y67_9FLAV	Q58Y67 dengue v1ru
52	53	100.0	3391	2	Q58Y69_9FLAV	Q58Y69 dengue v1ru
53	53	100.0	3391	2	Q58Y71_9FLAV	Q58Y71 dengue v1ru
54	53	100.0	3391	2	Q8QR27_9FLAV	Q8QR27 dengue v1ru
55	53	100.0	3391	2	Q91SD1_9FLAV	Q91SD1 dengue v1ru
56	53	100.0	3391	2	Q91F59_9FLAV	Q91F59 dengue v1ru
57	53	100.0	3391	2	Q91F59_9FLAV	Q91F59 dengue v1ru
58	53	100.0	3391	2	Q91SD1_9FLAV	Q91SD1 dengue v1ru
59	53	100.0	3391	2	Q91SD2_9FLAV	Q91SD2 dengue v1ru
60	53	100.0	3391	2	Q91SD3_9FLAV	Q91SD3 dengue v1ru
61	53	100.0	3391	2	Q91SD4_9FLAV	Q91SD4 dengue v1ru
62	53	100.0	3391	2	Q91SD5_9FLAV	Q91SD5 dengue v1ru
63	53	100.0	3391	2	Q91SD6_9FLAV	Q91SD6 dengue v1ru
64	53	100.0	3391	2	Q91SD7_9FLAV	Q91SD7 dengue v1ru
65	53	100.0	3391	2	Q91SD8_9FLAV	Q91SD8 dengue v1ru
66	53	100.0	3391	2	Q91SD9_9FLAV	Q91SD9 dengue v1ru
67	53	100.0	3391	2	Q91SD0_9FLAV	Q91SD0 dengue v1ru
68	53	100.0	3391	2	Q91SD1_9FLAV	Q91SD1 dengue v1ru
69	53	100.0	3391	2	Q91SD2_9FLAV	Q91SD2 dengue v1ru
70	53	100.0	3391	2	Q91SD3_9FLAV	Q91SD3 dengue v1ru
71	53	100.0	3391	2	Q91SD4_9FLAV	Q91SD4 dengue v1ru
72	53	100.0	3391	2	Q91SD5_9FLAV	Q91SD5 dengue v1ru

73	53	100.0	3391	2	Q5WDA0_9FLAV	Q5WDA0 dengue v1ru
74	53	100.0	3391	2	Q5WDA1_9FLAV	Q5WDA1 dengue v1ru
75	53	100.0	3391	2	Q5WDA2_9FLAV	Q5WDA2 dengue v1ru
76	53	100.0	3391	2	Q5WDA3_9FLAV	Q5WDA3 dengue v1ru
77	53	100.0	3391	2	Q5WDA4_9FLAV	Q5WDA4 dengue v1ru
78	53	100.0	3391	2	Q5WDA5_9FLAV	Q5WDA5 dengue v1ru
79	53	100.0	3391	2	Q5WDA6_9FLAV	Q5WDA6 dengue v1ru
80	53	100.0	3391	2	Q5WDA7_9FLAV	Q5WDA7 dengue v1ru
81	53	100.0	3391	2	Q5WDA8_9FLAV	Q5WDA8 dengue v1ru
82	53	100.0	3391	2	Q5WDA9_9FLAV	Q5WDA9 dengue v1ru
83	53	100.0	3391	2	Q5WDA10_9FLAV	Q5WDA10 dengue v1ru
84	53	100.0	3391	2	Q5WDA11_9FLAV	Q5WDA11 dengue v1ru
85	53	100.0	3391	2	Q5WDA12_9FLAV	Q5WDA12 dengue v1ru
86	53	100.0	3391	2	Q5WDA13_9FLAV	Q5WDA13 dengue v1ru
87	53	100.0	3391	2	Q5WDA14_9FLAV	Q5WDA14 dengue v1ru
88	53	100.0	3391	2	Q5WDA15_9FLAV	Q5WDA15 dengue v1ru
89	53	100.0	3391	2	Q5WDA16_9FLAV	Q5WDA16 dengue v1ru
90	53	100.0	3391	2	Q5WDA17_9FLAV	Q5WDA17 dengue v1ru
91	52	98.1	775	2	Q5WDA18_9FLAV	Q5WDA18 dengue v1ru
92	52	98.1	3391	2	Q5WDA19_9FLAV	Q5WDA19 dengue v1ru
93	52	98.1	3391	2	Q5WDA20_9FLAV	Q5WDA20 dengue v1ru
94	52	98.1	3391	2	Q5WDA21_9FLAV	Q5WDA21 dengue v1ru
95	52	98.1	3391	2	Q5WDA22_9FLAV	Q5WDA22 dengue v1ru
96	52	98.1	3391	2	Q5WDA23_9FLAV	Q5WDA23 dengue v1ru
97	52	98.1	3391	2	Q5WDA24_9FLAV	Q5WDA24 dengue v1ru
98	51	96.2	3392	2	Q5WDA25_9FLAV	Q5WDA25 dengue v1ru
99	50	94.3	166	2	Q5WDA26_9FLAV	Q5WDA26 dengue v1ru
100	50	94.3	166	2	Q5WDA27_9FLAV	Q5WDA27 dengue v1ru
101	50	94.3	166	2	Q5WDA28_9FLAV	Q5WDA28 dengue v1ru
102	50	94.3	1127	1	POLG_DBN2	P30026 dengue v1ru
103	48	90.6	577	2	Q5WDA29_9FLAV	Q5WDA29 dengue v1ru
104	48	90.6	661	2	Q5WDA30_9FLAV	Q5WDA30 dengue v1ru
105	47	88.7	320	2	Q5WDA31_9FLAV	Q5WDA31 dengue v1ru
106	47	88.7	321	2	Q5WDA32_9FLAV	Q5WDA32 dengue v1ru
107	47	88.7	321	2	Q5WDA33_9FLAV	Q5WDA33 dengue v1ru
108	47	88.7	321	2	Q5WDA34_9FLAV	Q5WDA34 dengue v1ru
109	47	88.7	321	2	Q5WDA35_9FLAV	Q5WDA35 dengue v1ru
110	47	88.7	321	2	Q5WDA36_9FLAV	Q5WDA36 dengue v1ru
111	47	88.7	321	2	Q5WDA37_9FLAV	Q5WDA37 dengue v1ru
112	47	88.7	321	2	Q5WDA38_9FLAV	Q5WDA38 dengue v1ru
113	47	88.7	321	2	Q5WDA39_9FLAV	Q5WDA39 dengue v1ru
114	47	88.7	321	2	Q5WDA40_9FLAV	Q5WDA40 dengue v1ru
115	47	88.7	321	2	Q5WDA41_9FLAV	Q5WDA41 dengue v1ru
116	47	88.7	321	2	Q5WDA42_9FLAV	Q5WDA42 dengue v1ru
117	47	88.7	321	2	Q5WDA43_9FLAV	Q5WDA43 dengue v1ru
118	47	88.7	321	2	Q5WDA44_9FLAV	Q5WDA44 dengue v1ru
119	47	88.7	321	2	Q5WDA45_9FLAV	Q5WDA45 dengue v1ru
120	47	88.7	321	2	Q5WDA46_9FLAV	Q5WDA46 dengue v1ru
121	47	88.7	321	2	Q5WDA47_9FLAV	Q5WDA47 dengue v1ru
122	47	88.7	321	2	Q5WDA48_9FLAV	Q5WDA48 dengue v1ru
123	47	88.7	321	2	Q5WDA49_9FLAV	Q5WDA49 dengue v1ru
124	47	88.7	321	2	Q5WDA50_9FLAV	Q5WDA50 dengue v1ru
125	47	88.7	321	2	Q5WDA51_9FLAV	Q5WDA51 dengue v1ru
126	47	88.7	321	2	Q5WDA52_9FLAV	Q5WDA52 dengue v1ru
127	47	88.7	321	2	Q5WDA53_9FLAV	Q5WDA53 dengue v1ru
128	47	88.7	321	2	Q5WDA54_9FLAV	Q5WDA54 dengue v1ru

129	47	88.7	321	2	Q7A15_DEN3	Q7A15 dengue v1ru
130	47	88.7	321	2	Q7A16_DEN3	Q7A16 dengue v1ru
131	47	88.7	321	2	Q7A17_DEN3	Q7A17 dengue v1ru
132	47	88.7	321	2	Q7A18_DEN3	Q7A18 dengue v1ru
133	47	88.7	321	2	Q7A19_DEN3	Q7A19 dengue v1ru
134	47	88.7	321	2	Q7A20_DEN3	Q7A20 dengue v1ru
135	47	88.7	321	2	Q7A21_DEN3	Q7A21 dengue v1ru
136	47	88.7	321	2	Q7A22_DEN3	Q7A22 dengue v1ru
137	47	88.7	321	2	Q7A23_DEN3	Q7A23 dengue v1ru
138	47	88.7	321	2	Q7A24_DEN3	Q7A24 dengue v1ru
139	47	88.7	321	2	Q7A25_DEN3	Q7A25 dengue v1ru
140	47	88.7	321	2	Q7A26_DEN3	Q7A26 dengue v1ru
141	47	88.7	321	2	Q7A27_DEN3	Q7A27 dengue v1ru
142	47	88.7	321	2	Q7A28_DEN3	Q7A28 dengue v1ru
143	47	88.7	321	2	Q7A29_DEN3	Q7A29 dengue v1ru
144	47	88.7	321	2	Q7A30_DEN3	Q7A30 dengue v1ru
145	47	88.7	321	2	Q7A31_DEN3	Q7A31 dengue v1ru
146	47	88.7	321	2	Q7A32_DEN3	Q7A32 dengue v1ru
147	47	88.7	321	2	Q7A33_DEN3	Q7A33 dengue v1ru
148	47	88.7	321	2	Q7A34_DEN3	Q7A34 dengue v1ru
149	47	88.7	321	2	Q7A35_DEN3	Q7A35 dengue v1ru
150	47	88.7	321	2	Q7A36_DEN3	Q7A36 dengue v1ru

ALIGNMENTS

RESULT 1						
Q67424_9FLAV						
ID	Q67424_9FLAV	PRELIMINARY;	PRT;	120	AA.	
AC	Q67424_9FLAV	01-NOV-1996 (TRENBLER, 01, Created)				
DT	01-NOV-1996	(TRENBLER, 01, Last sequence update)				
DT	01-JUN-2003	(TRENBLER, 24, Last annotation update)				
DE	Genomic RNA for envelope protein E N-term. (Fragment).					
OS	Dengue virus type 2.					
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;					
OX	NCBI_TaxID=11060;					
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=New Guinea C;					
RX	MEDLINE=87197230; PubMed=2952760;					
RA	Biedrzycka A., Cauchl M.R., Bartholomaeus A., Gorman J.J.,					
RA	Wright P.J.;					
RT	"Characterization of protease cleavage sites involved in the formation					
RT	of the envelope glycoprotein and three non-structural proteins of					
RL	J. Gen. Virol. 68:1317-1326(1987)."					
DR	EMBL; X05375; CAA28966.1; -; Genomic_RNA.					
DR	HSP; Q86653; IOKE.					
DR	GO; GO:0019028; C:Viral capsid; IEA.					
DR	GO; GO:0019058; P:Viral infectious cycle; IEA.					
DR	InterPro; IPR011999; Flav1_glycoE_cen.					
DR	InterPro; IPR000069; Flav1_M.					
DR	InterPro; IPR011998; Viral_glycoE_cen.					


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RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21571640; PubMed=11714970;
RA Uzategui N.Y., Camacho D., Comacho G., Cuello de Uzategui R.,
RA Holmes E.C., Gould E.A.;
RT "Molecular epidemiology of dengue type 2 virus in Venezuela: evidence
RT for in situ virus evolution and recombination.";
RL J. Gen. Virol. 82:2945-2953(2001).
DR EMBL; AF360862; AAL76290.1; -; Genomic_RNA.
DR SMR; Q8Q265; 21-100.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; P:viral infectious cycle; IEA.
DR InterPro; IPR001122; Flavi_capsidC.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR002535; Flavi_propep.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR Polyprotein.
DR NON_TER
SQ SEQUENCE 280 AA; 31848 MW; BEB9F24ABD29CFBD CRC64;

Query Match 100.0%; Score 53; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
Db 237 IETWILRHP 245

RESULT 5
Q8Q266_9FLAV
ID Q8Q266_9FLAV PRELIMINARY; PRT; 280 AA.
AC Q8Q266;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polyprotein (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxID=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21571640; PubMed=11714970;
RA Uzategui N.Y., Camacho D., Comacho G., Cuello de Uzategui R.,
RA Holmes E.C., Gould E.A.;
RT "Molecular epidemiology of dengue type 2 virus in Venezuela: evidence
RT for in situ virus evolution and recombination.";
RL J. Gen. Virol. 82:2945-2953(2001).
DR EMBL; AF360861; AAL76289.1; -; Genomic_RNA.
DR SMR; Q8Q266; 21-100.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; P:viral infectious cycle; IEA.

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DR InterPro; IPR001122; Flavi_capsidC.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR002535; Flavi_propep.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR Polyprotein.
DR NON_TER
SQ SEQUENCE 280 AA; 31892 MW; 814AB9B4A22AC20 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
Db 237 IETWILRHP 245

RESULT 6
Q8Q267_9FLAV
ID Q8Q267_9FLAV PRELIMINARY; PRT; 280 AA.
AC Q8Q267;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polyprotein (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxID=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21571640; PubMed=11714970;
RA Uzategui N.Y., Camacho D., Comacho G., Cuello de Uzategui R.,
RA Holmes E.C., Gould E.A.;
RT "Molecular epidemiology of dengue type 2 virus in Venezuela: evidence
RT for in situ virus evolution and recombination.";
RL J. Gen. Virol. 82:2945-2953(2001).
DR EMBL; AF360860; AAL76288.1; -; Genomic_RNA.
DR SMR; Q8Q267; 21-100.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; P:viral infectious cycle; IEA.
DR InterPro; IPR001122; Flavi_capsidC.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR002535; Flavi_propep.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR Polyprotein.
DR NON_TER
SQ SEQUENCE 280 AA; 31892 MW; 814AB9B4A22AC20 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 IETWLRHP 9
Db 237 IETWLRHP 245

RESULT 7

POLC_DENZH STANDARD; PRT; 555 AA.
ID POLC_DENZH
AC P29984;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Genome polyprotein [Contains: Envelope protein M (Matrix protein);
Major envelope protein E; Nonstructural protein 1 (NS1) (Fragment).
OS Dengue virus type 2 (strain TH-36).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
NC NCB1_TaxID=316377;
RN (1)
RP NUCLEOTIDE SEQUENCE (GENOMIC RNA).
RX MEDLINE=92113574; PubMed=1339466;
RA Shiu S.Y.W., Jiang W.R., Porterfield J.S., Gould E.A.;
RT "Envelope protein sequences of dengue virus isolates TH-36 and TH-
Smant, and identification of a type-specific genetic marker for dengue
and tick-borne flaviviruses.";
RL J. Gen. Virol. 73:207-212(1992).
CC -1- PTM: Specific enzymatic cleavages in vivo yield mature proteins
(By similarity).
CC -1- MISCELLANEOUS: The virion of this virus is a nucleocapsid covered
by a lipoprotein envelope. The envelope contains two proteins: the
protein M and glycoprotein E. The nucleocapsid is a complex of
protein C and mRNA. In immature particles, there are 60
icosahedrally organized trimeric spikes on the surface. Each spike
consists of three heterodimers of envelope protein M precursor
(prM) and envelope protein E (By similarity).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; D10514; BAA01389.1; -; Genomic_RNA.
DR PIR; J01404; J01404.
DR HSSP; Q88653; 10KE.
DR SMR; P29984; 50-443.
DR InterPro; IPR011999; Flavi_glycoE_cen.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR000336; Flv_glyE_1g-like.
DR InterPro; IPR011998; Viral_glycoE_cen.
DR Pfam; PF02832; Flavi_glycopr_C; 1.
DR Pfam; PF00869; Flavi_glycopr_C; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR ProDom; PD001556; Flavi_glycoprE; 1.
KW Capsid protein; Core protein; Envelope protein; Glycoprotein;
KW Polyprotein; Structural protein; Transmembrane.

FT CHAIN <1 49 Envelope protein M.
FT CHAIN 50 544 Major envelope protein E.
FT CHAIN 545 >555 Nonstructural protein 1.
FT TRANSMEM 37 53 Potential.
FT TRANSMEM 496 512 Potential.
FT TRANSMEM 526 542 Potential.
FT CARBOHYD 116 116 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 202 202 N-linked (GlcNAc...) (Potential).
FT DISULFID 32 79 By similarity.
FT DISULFID 109 170 By similarity.
FT DISULFID 123 154 By similarity.
FT DISULFID 141 165 By similarity.
FT DISULFID 234 334 By similarity.
FT DISULFID 351 382 By similarity.
FT NON_TER 1 1
FT NON_TER 555 555
SQ SEQUENCE 555 AA; 61243 MW; F9DEA740BB4DBDF CRC64;

Query Match 100.0%; Score 53; DB 1; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWLRHP 9
Db 6 IETWLRHP 14

RESULT 8

012290_9FLAV
ID 012290_9FLAV PRELIMINARY; PRT; 578 AA.
AC 012290;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
NC NCB1_TaxID=11060;
RN (1)
RP STRAIN=Torres Strait 1;
RC NUCLEOTIDE SEQUENCE.
RA Serafin I.L., Phillips D.A.;
RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF004019; AAB61366.1; -; mRNA.
DR HSSP; Q88653; 10KE.
DR SMR; 012290; 48-441.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; P:viral infectious cycle; IEA.
DR InterPro; IPR011999; Flavi_glycoE_cen.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR001157; Flavi_NS1.
DR InterPro; IPR000336; Flv_glyE_1g-like.
DR InterPro; IPR011998; Viral_glycoE_cen.
DR Pfam; PF00869; Flavi_glycopr_C; 1.

DR Pfam: PF02832; Flavi_glycop_C; 1.
DR Pfam: PF01004; Flavi_M; 1.
DR Pfam: PF00948; Flavi_NSI; 1.
DR ProDom: PD001556; Flavi_glycoprote; 1.
DR ProDom: PD001496; Flavi_NSI; 1.
KW Polypeptidn.
FT CHAIN <1 47 membrane protein.
FT CHAIN 48 542 envelope protein.
FT CHAIN 543 >578 nonstructural protein 1.
FT NON_TER 1 1
FT NON_TER 578 578
SQ SEQUENCE 578 AA; 63605 MW; 1C03A7CFD72C567D CRC64;

Query Match 100.0%; Score 53; DB 2; Length 578;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
DB 4 IETWILRHP 12

RESULT 9

ID Q501B6_9FLAV PRELIMINARY; PRT; 661 AA.
AC Q501B6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Polypeptidn (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxID=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BCL34-Merida-94;
RX PubMed=15316647;
RA Llorono-Pino M.A., Farfan-Ale J.A., Zapata-Peraza A.L.,
RA Rosado-Paredes E.P., Flores-Flores L.F., Garcia-Rejon J., Diaz F.J.,
RA Blitvich B.J., Jimenez-Rios E., Blair C.D., Olson K.E., Black W. IV,
RA Beatty B.J.;
RT "Introduction of the American/Asian genotype of dengue 2 virus into
the Yucatan State of Mexico.";
RL Am. J. Trop. Med. Hyg. 71:485-492(2004).
DR EMBL: AY466449; AAS45234.1; -; mRNA.
DR SMR: Q501B6; 167-560.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0019058; F:viral infectious cycle; IEA.
DR InterPro: IPR001999; Flavi_glycop_cen.
DR InterPro: IPR000069; Flavi_M.
DR InterPro: IPR002535; Flavi_glycop.
DR InterPro: IPR000336; Flv_glyc_1g-like.
DR InterPro: IPR011998; Viral_glycop_cen.
DR Pfam: PF00869; Flavi_glycoprot; 1.

DR Pfam: PF02832; Flavi_glycop_C; 1.
DR Pfam: PF01004; Flavi_M; 1.
DR Pfam: PF01570; Flavi_propep; 1.
DR ProDom: PD001556; Flavi_glycoprote; 1.
KW Polypeptidn.
FT NON_TER 1 1
FT NON_TER 661 661
SQ SEQUENCE 661 AA; 73206 MW; A919612986E04157 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
DB 123 IETWILRHP 131

RESULT 10

ID Q5V187_9FLAV PRELIMINARY; PRT; 661 AA.
AC Q5V187;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Polypeptidn (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxID=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=13382/Tizimih 02;
RX PubMed=15316647;
RA Llorono-Pino M.A., Farfan-Ale J.A., Zapata-Peraza A.L.,
RA Rosado-Paredes E.P., Flores-Flores L.F., Garcia-Rejon J., Diaz F.J.,
RA Blitvich B.J., Jimenez-Rios E., Blair C.D., Olson K.E., Black W. IV,
RA Beatty B.J.;
RT "Introduction of the American/Asian genotype of dengue 2 virus into
the Yucatan State of Mexico.";
RL Am. J. Trop. Med. Hyg. 71:485-492(2004).
DR EMBL: AY449684; AAS14975.1; -; Genomic_RNA.
DR SMR: Q5V187; 167-560.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0019058; F:viral infectious cycle; IEA.
DR InterPro: IPR011999; Flavi_glycop_cen.
DR InterPro: IPR000069; Flavi_M.
DR InterPro: IPR002535; Flavi_glycop.
DR InterPro: IPR000336; Flv_glyc_1g-like.
DR InterPro: IPR011998; Viral_glycop_cen.
DR Pfam: PF00869; Flavi_glycoprot; 1.
DR Pfam: PF02832; Flavi_glycop_C; 1.
DR Pfam: PF01004; Flavi_M; 1.
DR Pfam: PF01570; Flavi_propep; 1.
DR ProDom: PD001556; Flavi_glycoprote; 1.

KW Polypeptidn. 1 1
FT NON_TER 661 661
SQ SEQUENCE 661 AA; 73118 MW; CE2051C17F40A623 CRC64;
Query Match 100.0%; Score 53; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IETWILRHP 9
Db 123 IETWILRHP 131
RESULT 11
QSV188_9FLAV PRELIMINARY; PRT; 661 AA.
ID QSV188_9FLAV PRELIMINARY;
AC QSV188;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Polypeptidn (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxID=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=13381/Chochoila 02;
RX PubMed=15516647;
RA Lotono-Pino M.A., Farfan-Ale J.A., Zapata-Peraza A.L.,
RA Rosado-Parades E.P., Flores-Flores L.F., Garcia-Rejon J., Diaz F.J.,
RA Biltvich B.J., Jimenez-Rios E., Blair C.D., Olson K.E., Black W. IV,
RA Beatty B.J.;
RT "Introduction of the American/Asian genotype of dengue 2 virus into
the Yucatan State of Mexico.";
RL Am. J. Trop. Med. Hyg. 71:485-492(2004).
DR EMBL; AY449683; AAS14974.1; -; genomic_RNA.
DR SMR; QSV188; 167-560.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; P:viral infectious cycle; IEA.
DR InterPro; IPR011999; Flavi_glycoE_cen.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR002535; Flavi_propep.
DR InterPro; IPR000336; Flv_glyE_Ig-like.
DR InterPro; IPR011998; Viral_glycoE_cen.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR Pfam; PD001556; Flavi_glycoprote; 1.
KW Polypeptidn.
FT NON_TER 1 1
FT NON_TER 661 661
SQ SEQUENCE 661 AA; 73092 MW; 482C14A6B3B179FA CRC64;

Query Match 100.0%; Score 53; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IETWILRHP 9
Db 123 IETWILRHP 131
RESULT 12
QSV189_9FLAV
ID QSV189_9FLAV PRELIMINARY; PRT; 661 AA.
AC QSV189;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Polypeptidn (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxID=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12021/Oukutzcab 01;
RX PubMed=15516647;
RA Lotono-Pino M.A., Farfan-Ale J.A., Zapata-Peraza A.L.,
RA Rosado-Parades E.P., Flores-Flores L.F., Garcia-Rejon J., Diaz F.J.,
RA Biltvich B.J., Jimenez-Rios E., Blair C.D., Olson K.E., Black W. IV,
RA Beatty B.J.;
RT "Introduction of the American/Asian genotype of dengue 2 virus into
the Yucatan State of Mexico.";
RL Am. J. Trop. Med. Hyg. 71:485-492(2004).
DR EMBL; AY449682; AAS14973.1; -; genomic_RNA.
DR SMR; QSV189; 167-560.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; P:viral infectious cycle; IEA.
DR InterPro; IPR011999; Flavi_glycoE_cen.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR002535; Flavi_propep.
DR InterPro; IPR000336; Flv_glyE_Ig-like.
DR InterPro; IPR011998; Viral_glycoE_cen.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR Pfam; PD001556; Flavi_glycoprote; 1.
KW Polypeptidn.
FT NON_TER 1 1
FT NON_TER 661 661
SQ SEQUENCE 661 AA; 73080 MW; 5216054D684173C0 CRC64;
Query Match 100.0%; Score 53; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
|||||
Db 123 IETWILRHP 131

RESULT 13

OSV190_9FLAV PRELIMINARY; PRT; 661 AA.
ID OSV190_9FLAV
AC OSV190;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, last annotation update)
DE Polyprotein (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxId=11060;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=11936/St. Elena 01;
RX PubMed=15116647;
RA Llorono-Pino M.A., Farfan-Ale J.A., Zapata-Peraza A.L.,
RA Rosado-Parades E.P., Flores-Flores L.F., Garcia-Rejon J., Diaz F.J.,
RA Blitvich B.J., Jimenez-Rios E., Blatr C.D., Olson K.E., Black W. IV,
RA Beatty B.J.;
RT "Introduction of the American/Asian genotype of dengue 2 virus into
the Yucatan State of Mexico."
RL Am. J. Trop. Med. Hyg. 71:485-492(2004).
DR EMBL: AY449681; AAS14972.1; -; Genomic_RNA.
DR SMR: OSV190; 167-560.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0019058; P:viral infectious cycle; IEA.
DR InterPro: IPR011999; Flavi_glycoE_cen.
DR InterPro: IPR000069; Flavi_M.
DR InterPro: IPR002353; Flavi_propep.
DR InterPro: IPR000336; Flv_glyE_1g-1like.
DR InterPro: IPR011998; Viral_glycoE_cen.
DR Pfam: PF00869; Flavi_glycoprot; 1.
DR Pfam: PF02832; Flavi_glycop_C; 1.
DR Pfam: PF01004; Flavi_M; 1.
DR Pfam: PF01570; Flavi_propep; 1.
DR ProDom: PD001556; Flavi_glycoprote; 1.
KW Polyprotein.
FT NON_TER 1 1
FT NON_TER 661 661
SQ SEQUENCE 661 AA; 73080 MW; 5216054D684173C0 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IETWILRHP 9
|||||
Db 123 IETWILRHP 131

RESULT 14
OSV191_9FLAV PRELIMINARY; PRT; 661 AA.
ID OSV191_9FLAV
AC OSV191;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, last annotation update)
DE Polyprotein (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxId=11060;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12914/Tekax 01;
RX PubMed=15116647;
RA Llorono-Pino M.A., Farfan-Ale J.A., Zapata-Peraza A.L.,
RA Rosado-Parades E.P., Flores-Flores L.F., Garcia-Rejon J., Diaz F.J.,
RA Blitvich B.J., Jimenez-Rios E., Blatr C.D., Olson K.E., Black W. IV,
RA Beatty B.J.;
RT "Introduction of the American/Asian genotype of dengue 2 virus into
the Yucatan State of Mexico."
RL Am. J. Trop. Med. Hyg. 71:485-492(2004).
DR EMBL: AY449680; AAS14971.1; -; Genomic_RNA.
DR SMR: OSV191; 167-560.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0019058; P:viral infectious cycle; IEA.
DR InterPro: IPR011999; Flavi_glycoE_cen.
DR InterPro: IPR000069; Flavi_M.
DR InterPro: IPR002353; Flavi_propep.
DR InterPro: IPR000336; Flv_glyE_1g-1like.
DR InterPro: IPR011998; Viral_glycoE_cen.
DR Pfam: PF00869; Flavi_glycoprot; 1.
DR Pfam: PF02832; Flavi_glycop_C; 1.
DR Pfam: PF01004; Flavi_M; 1.
DR Pfam: PF01570; Flavi_propep; 1.
DR ProDom: PD001556; Flavi_glycoprote; 1.
KW Polyprotein.
FT NON_TER 1 1
FT NON_TER 661 661
SQ SEQUENCE 661 AA; 73080 MW; 5216054D684173C0 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IETWILRHP 9
|||||
Db 123 IETWILRHP 131

RESULT 15
OSV192_9FLAV

ID 05V192_9FLAV PRELIMINARY; PRT; 661 AA.
AC 05V192;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Polypeptide (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxId=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C1077/Chilpancingo 97;
RX PubMed=15516647;
RA Latoro-Pino M.A., Farfan-Ale J.A., Zapata-Perez A.L., Diaz F.J.,
RA Rosado-Paredes E.P., Flores-Flores L.F., Garcia-Rejon J., Blair C.D., Olson K.E., Black W. IV,
RA Blitvich B.J., Jimenez-Rios E., Blair C.D., Olson K.E., Black W. IV,
RA Beatty B.J.;
RT "Introduction of the American/Asian genotype of dengue 2 virus into
the Yucatan State of Mexico.";
RL Am. J. Trop. Med. Hyg. 71:485-492(2004).
DR EMBL; AY449679; AAS14970.1; -; Genomic_RNA.
DR SMR; 05V192; 167-560.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; P:viral infectious cycle; IEA.
DR InterPro; IPR011999; Flavi_glycof_cen.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR002535; Flavi_propep.
DR InterPro; IPR000336; Flv_glye_1g-like.
DR InterPro; IPR011998; Viral_glycof_cen.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycoprot; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
KW Polypeptid.
FT NON_TER 1
FT NON_TER 661
SQ SEQUENCE 661 AA; 73023 MW; 367D6F1A9F25932B CRC64;

Query Match 100.0%; Score 53; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 IETWLRHP 9
|||||
DB 123 IETWLRHP 131

RESULT 16
05V193_9FLAV PRELIMINARY; PRT; 661 AA.
ID 05V193;
AC 05V193;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Polypeptide (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxId=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C-932/Acapulco 97;
RX PubMed=15516647;
RA Latoro-Pino M.A., Farfan-Ale J.A., Zapata-Perez A.L., Diaz F.J.,
RA Rosado-Paredes E.P., Flores-Flores L.F., Garcia-Rejon J., Blair C.D., Olson K.E., Black W. IV,
RA Blitvich B.J., Jimenez-Rios E., Blair C.D., Olson K.E., Black W. IV,
RA Beatty B.J.;
RT "Introduction of the American/Asian genotype of dengue 2 virus into
the Yucatan State of Mexico.";
RL Am. J. Trop. Med. Hyg. 71:485-492(2004).
DR EMBL; AY449678; AAS14969.1; -; Genomic_RNA.
DR SMR; 05V193; 167-560.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; P:viral infectious cycle; IEA.
DR InterPro; IPR011999; Flavi_glycof_cen.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR002535; Flavi_propep.
DR InterPro; IPR000336; Flv_glye_1g-like.
DR InterPro; IPR011998; Viral_glycof_cen.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycoprot; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
KW Polypeptid.
FT NON_TER 1
FT NON_TER 661
SQ SEQUENCE 661 AA; 73024 MW; 0E74A2AC438791A1 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 IETWLRHP 9
|||||
DB 123 IETWLRHP 131

RESULT 17
05V194_9FLAV PRELIMINARY; PRT; 661 AA.
ID 05V194;
AC 05V194;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Polypeptide (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Flavivirus; Dengue virus group.
 OX NCBI_TaxID=11060;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BC17/Merida 96;
 RA Rosado-Paredes E.P., Flores-Flores L.F., Garcia-Rejon J., Diaz F.J.,
 RA Blitvich B.J., Jimenez-Rios E., Blair C.D., Olson K.E., Black W. IV,
 RA Beatty B.J.;
 RT "Introduction of the American/Asian genotype of dengue 2 virus into
 the Yucatan State of Mexico.";
 RL Am. J. Trop. Med. Hyg. 71:485-492(2004).
 DR EMBL: AY449677; AAS14968.1; -; Genomic_RNA.
 DR SMR: Q5V195; 167-560.
 DR GO: GO:0019028; C:viral capsid; IEA.
 DR GO: GO:0019031; C:viral envelope; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR GO: GO:0019058; P:viral infectious cycle; IEA.
 DR InterPro: IPR011999; Flavi_glycop_cen.
 DR InterPro: IPR000069; Flavi_M.
 DR InterPro: IPR002535; Flavi_propep.
 DR InterPro: IPR000336; Flv_glyc_1g-like.
 DR InterPro: IPR011998; Viral_glycop_cen.
 DR Pfam: PF00869; Flavi_glycoprot; 1.
 DR Pfam: PF02832; Flavi_glycop_C; 1.
 DR Pfam: PF01004; Flavi_M; 1.
 DR Pfam: PF01570; Flavi_propep; 1.
 DR Prodom: PD001556; Flavi_glycoprote; 1.
 KM Polypeptin.
 FT NON_TER 1 1
 FT NON_TER 661 661
 SQ SEQUENCE 661 AA; 73056 MW; 7CA5BA842F2CA044 CRC64;

 Query Match 100.0%; Score 53; DB 2; Length 661;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 1ETWILRHP 9
 DB 123 1ETWILRHP 131

 RESULT 18
 Q5V195_9FLAV
 ID Q5V195_9FLAV PRELIMINARY; PRT; 661 AA.
 AC Q5V195;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DE Polypeptin (Fragment).
 OS Dengue virus type 2.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus; Dengue virus group.
 OX NCBI_TaxID=11060;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BC139/Quintana Roo 94;
 RX PubMed=15516647;
 RA Llorono-Pino M.A., Farfan-Ale J.A., Zapata-Peraza A.L.,
 RA Rosado-Paredes E.P., Flores-Flores L.F., Garcia-Rejon J., Diaz F.J.,
 RA Blitvich B.J., Jimenez-Rios E., Blair C.D., Olson K.E., Black W. IV,
 RA Beatty B.J.;
 RT "Introduction of the American/Asian genotype of dengue 2 virus into
 the Yucatan State of Mexico.";
 RL Am. J. Trop. Med. Hyg. 71:485-492(2004).
 DR EMBL: AY449676; AAS14967.1; -; Genomic_RNA.
 DR SMR: Q5V195; 167-560.
 DR GO: GO:0019028; C:viral capsid; IEA.
 DR GO: GO:0019031; C:viral envelope; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR GO: GO:0019058; P:viral infectious cycle; IEA.
 DR InterPro: IPR011999; Flavi_glycop_cen.
 DR InterPro: IPR000069; Flavi_M.
 DR InterPro: IPR002535; Flavi_propep.
 DR InterPro: IPR000336; Flv_glyc_1g-like.
 DR InterPro: IPR011998; Viral_glycop_cen.
 DR Pfam: PF00869; Flavi_glycoprot; 1.
 DR Pfam: PF02832; Flavi_glycop_C; 1.
 DR Pfam: PF01004; Flavi_M; 1.
 DR Pfam: PF01570; Flavi_propep; 1.
 DR Prodom: PD001556; Flavi_glycoprote; 1.
 KM Polypeptin.
 FT NON_TER 1 1
 FT NON_TER 661 661
 SQ SEQUENCE 661 AA; 73120 MW; 2F4A06810C54EFAD CRC64;

 Query Match 100.0%; Score 53; DB 2; Length 661;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 1ETWILRHP 9
 DB 123 1ETWILRHP 131

 RESULT 19
 Q5V196_9FLAV
 ID Q5V196_9FLAV PRELIMINARY; PRT; 661 AA.
 AC Q5V196;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DE Polypeptin (Fragment).
 OS Dengue virus type 2.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus; Dengue virus group.
 OX NCBI_TaxID=11060;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SU1482/Mexico 84;
 RX PubMed=15516647;
 RA Llorono-Pino M.A., Farfan-Ale J.A., Zapata-Peraza A.L.,
 RA Rosado-Paredes E.P., Flores-Flores L.F., Garcia-Rejon J., Diaz F.J.,

RA Blilevich B.J., Jimenez-Rios E., Blair C.D., Olson K.E., Black W. IV,
RA Beatty B.J.:
RT "Introduction of the American/Asian genotype of dengue 2 virus into
the Yucatan State of Mexico.";
RL Am. J. Trop. Med. Hyg. 71:485-492(2004).
DR EMBL: AY449675; AAS14966.1; -; Genomic_RNA.
DR SMR: OSV196; 167-560.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0019058; P:viral infectious cycle; IEA.
DR InterPro: IPR011999; Flavi_glycof_cen.
DR InterPro: IPR000069; Flavi_M.
DR InterPro: IPR002535; Flavi_propep.
DR InterPro: IPR000336; Flv_glye_19-like.
DR InterPro: IPR011998; Viral_glycof_cen.
DR Pfam: PF00869; Flavi_glycoprot; 1.
DR Pfam: PF02832; Flavi_glycop_C; 1.
DR Pfam: PF01004; Flavi_M; 1.
DR Pfam: PF01570; Flavi_propep; 1.
DR ProDom: PD001556; Flavi_glycoprote; 1.
DR Polypeptidn.
FT NON_TER 1 1
SQ SEQUENCE 661 AA; 73210 MW; B2D61860739F94BB CRC64;

Query Match 100.0%; Score 53; DB 2; Length 661;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWLRHP 9
IIIIIIIIII

DB 123 IETWLRHP 131

RESULT 20
06DUV2_9FLAV PRELIMINARY; PRT; 716 AA.
AC 06DUV2;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Structural polyprotein (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCB1_TaxID=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cruz A.C.R., Vasconcelos P.F.C., Ferreira A.P., Vasconcelos H.B.,
RA Jabor A.V., da Rosa E.S.T., Gallier R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY642588; AAT58366.1; -; Genomic_RNA.
DR SMR: 06DUV2; 176-569.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.

DR GO: GO:0019058; P:viral infectious cycle; IEA.
DR InterPro: IPR011999; Flavi_glycof_cen.
DR InterPro: IPR000069; Flavi_M.
DR InterPro: IPR001157; Flavi_NS1.
DR InterPro: IPR002535; Flavi_propep.
DR InterPro: IPR000336; Flv_glye_19-like.
DR InterPro: IPR011998; Viral_glycof_cen.
DR Pfam: PF00869; Flavi_glycoprot; 1.
DR Pfam: PF02832; Flavi_glycop_C; 1.
DR Pfam: PF01004; Flavi_M; 1.
DR Pfam: PF00948; Flavi_NS1; 1.
DR Pfam: PF01570; Flavi_propep; 1.
DR ProDom: PD001556; Flavi_glycoprote; 1.
DR ProDom: PD001496; Flavi_NS1; 1.
DR Polypeptidn.
FT NON_TER 1 1
SQ SEQUENCE 716 AA; 79209 MW; DE2DA70891395C7F CRC64;

Query Match 100.0%; Score 53; DB 2; Length 716;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWLRHP 9
IIIIIIIIII

DB 132 IETWLRHP 140

RESULT 21
05ICU9_9FLAV PRELIMINARY; PRT; 724 AA.
AC 05ICU9;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Polypeptidn (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCB1_TaxID=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cruz A.C.R., Vasconcelos P.F.C., Ferreira A.P., Vasconcelos H.B.,
RA Jabor A.V., Travassos da Rosa E.S., Gallier R.;
RT "Genetic characterization of Dengue virus 2 and 3 isolated from
Brazil.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY778960; AAM51131.1; -; Genomic_RNA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0019058; P:viral infectious cycle; IEA.
DR InterPro: IPR011999; Flavi_glycof_cen.
DR InterPro: IPR000069; Flavi_M.
DR InterPro: IPR001157; Flavi_NS1.
DR InterPro: IPR002535; Flavi_propep; 1.

DR InterPro: IPR000336; Flv_glyc_1g-like.
DR InterPro: IPR01998; Viral_glycoE_cen.
DR Pfam: PF00869; Flavi_glycoprot; 1.
DR Pfam: PF02832; Flavi_glycop_C; 1.
DR Pfam: PF01004; Flavi_M; 1.
DR Pfam: PF00948; Flavi_NSI; 1.
DR Pfam: PF01570; Flavi_propep; 1.
DR ProDom: PD001556; Flavi_glycoprote; 1.
DR ProDom: PD001496; Flavi_NSI; 1.
DR PolyProtein.
KW Polypeptide.
FT NON_TER 1 1
FT NON_TER 724 724
SQ SEQUENCE 724 AA; 80036 MW; BD9377E53684D67 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 724;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IETWILRHP 9
|||||
Db 134 IETWILRHP 142

RESULT 22
Q58K9_9FLAV PRELIMINARY; PRT; 745 AA.
ID Q58K9_9FLAV PRELIMINARY;
AC Q58K9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Polypeptide (Fragment).
OS Dengue virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxID=12637;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bach Thi Q.N., Truong Uyen N., Truong Thua T., Le Thi M.Q.,
RA Nguyen Thi H.H., Dinh Duy K.;
RT "Cloning and expression of the gene coding for prem and envelope
RT protein of dengue virus typ 2.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ574886; CAE00500.1; -; Genomic_RNA.
DR SMR; Q58K9; 190-583.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; P:viral infectious cycle; IEA.
DR InterPro: IPR01999; Flavi_glycoE_cen.
DR InterPro: IPR00069; Flavi_M.
DR InterPro: IPR001157; Flavi_NSI.
DR InterPro: IPR002535; Flavi_propep.
DR InterPro: IPR000336; Flv_glyc_1g-like.
DR InterPro: IPR01998; Viral_glycoE_cen.
DR Pfam: PF00869; Flavi_glycoprot; 1.
DR Pfam: PF02832; Flavi_glycop_C; 1.
DR Pfam: PF01004; Flavi_M; 1.

DR Pfam: PF00948; Flavi_NSI; 1.
DR Pfam: PF01570; Flavi_propep; 1.
DR ProDom: PD001556; Flavi_glycoprote; 1.
DR ProDom: PD001496; Flavi_NSI; 1.
DR PolyProtein.
KW Polypeptide.
FT CHAIN 24 189 prem protein M.
FT CHAIN 190 684 envelope protein E.
FT CHAIN 685 744 non structural protein NS1.
FT NON_TER 1 1
FT NON_TER 745 745
SQ SEQUENCE 745 AA; 82433 MW; 91514AD61E91CF9E CRC64;

Query Match 100.0%; Score 53; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IETWILRHP 9
|||||
Db 146 IETWILRHP 154

RESULT 23
Q58P1_9FLAV PRELIMINARY; PRT; 757 AA.
ID Q58P1_9FLAV PRELIMINARY;
AC Q58P1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Structural polyprotein (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxID=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FOR1812;
RA Cruz A.C.R., Vasconcelos P.F.C., Ferreira A.P., Vasconcelos H.B.,
RA Jabor A.V., da Rosa E.S.T., Galler R.;
RT "Genetic characterization of Dengue virus type 2 and 3 from Brazil.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY714062; AAU93389.1; -; Genomic_RNA.
DR SMR; Q58P1; 213-606.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; P:viral infectious cycle; IEA.
DR InterPro: IPR01122; Flavi_capsidC.
DR InterPro: IPR01999; Flavi_glycoE_cen.
DR InterPro: IPR00069; Flavi_M.
DR InterPro: IPR001157; Flavi_NSI.
DR InterPro: IPR002535; Flavi_propep.
DR InterPro: IPR000336; Flv_glyc_1g-like.
DR InterPro: IPR01998; Viral_glycoE_cen.
DR Pfam: PF01003; Flavi_capsid; 1.
DR Pfam: PF00869; Flavi_glycoprot; 1.
DR Pfam: PF02832; Flavi_glycop_C; 1.
DR Pfam: PF01004; Flavi_M; 1.

DR Pfam: PF00948; Flavi_NSI; 1.
 DR Pfam: PF01570; Flavi_propep; 1.
 DR ProDom: PD001556; Flavi_glycoprote; 1.
 DR ProDom: PD001496; Flavi_NSI; 1.
 KW Polypeptin.
 FT NON_TER 1 1
 FT NON_TER 757 757
 SQ SEQUENCE 757 AA; 83836 MW; 28D2DAE7FE7C77AF CRC64;

Query Match 100.0%; Score 53; DB 2; Length 757;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRRP 9
 IIIIIIIIII
 Db 169 IETWILRRP 177

RESULT 24
 ID Q58P2_9FLAV PRELIMINARY; PRT; 757 AA.
 AC Q58P2;
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE Structural polyprotein (Fragment).
 OS Dengue virus type 2.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus; Dengue virus group.
 OX NCBI_TaxID=11060;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MG1269;
 RA Cruz A.C.R., Vasconcelos P.F.C., Ferreira A.P., Vasconcelos H.B.,
 RA Jabor A.V., da Rosa E.S.T., Gallier R.;
 RT "Genetic characterization of Dengue virus type 2 and 3 from Brazil.";
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY714061; AAU93388.1; -; Genomic_RNA.
 DR SMR; Q58P2; 213-606.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:viral infectious cycle; IEA.
 DR GO; GO:0019058; P:viral infectious cycle; IEA.
 DR InterPro: IPR001122; Flavi_capsidC.
 DR InterPro: IPR011999; Flavi_glycoC_en.
 DR InterPro: IPR000069; Flavi_M.
 DR InterPro: IPR001157; Flavi_NSI.
 DR InterPro: IPR002535; Flavi_propep.
 DR InterPro: IPR000336; Flv_glye_1g-1like.
 DR InterPro: IPR011998; Viral_glycoC_en.
 DR Pfam; PF01003; Flavi_capsid; 1.
 DR Pfam; PF00869; Flavi_glycoprot; 1.
 DR Pfam; PF02832; Flavi_glycop_C; 1.
 DR Pfam; PF01004; Flavi_M; 1.
 DR Pfam; PF00948; Flavi_NSI; 1.
 DR Pfam; PF01570; Flavi_propep; 1.
 DR ProDom; PD001556; Flavi_glycoprote; 1.

DR ProDom: PD001496; Flavi_NSI; 1.
 KW Polypeptin.
 FT NON_TER 1 1
 FT NON_TER 757 757
 SQ SEQUENCE 757 AA; 83859 MW; E32D6A1E6152F4F6 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 757;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRRP 9
 IIIIIIIIII
 Db 169 IETWILRRP 177

RESULT 25
 ID Q6DD9_9FLAV PRELIMINARY; PRT; 757 AA.
 AC Q6DD9;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Structural polyprotein (Fragment).
 OS Dengue virus type 2.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus; Dengue virus group.
 OX NCBI_TaxID=11060;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Cruz A.C.R., Vasconcelos P.F.C., Ferreira A.P., Vasconcelos H.B.,
 RA Jabor A.V., da Rosa E.S.T., Gallier R.;
 RL Submitted (Jun-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY644452; AAT68021.1; -; Genomic_RNA.
 DR SMR; Q6DD9; 213-606.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0019058; P:viral infectious cycle; IEA.
 DR InterPro: IPR001122; Flavi_capsidC.
 DR InterPro: IPR011999; Flavi_glycoC_en.
 DR InterPro: IPR000069; Flavi_M.
 DR InterPro: IPR001157; Flavi_NSI.
 DR InterPro: IPR002535; Flavi_propep.
 DR InterPro: IPR000336; Flv_glye_1g-1like.
 DR InterPro: IPR011998; Viral_glycoC_en.
 DR Pfam; PF01003; Flavi_capsid; 1.
 DR Pfam; PF00869; Flavi_glycoprot; 1.
 DR Pfam; PF02832; Flavi_glycop_C; 1.
 DR Pfam; PF01004; Flavi_M; 1.
 DR Pfam; PF00948; Flavi_NSI; 1.
 DR ProDom; PD001556; Flavi_glycoprote; 1.
 DR ProDom; PD001496; Flavi_NSI; 1.
 KW Polypeptin.
 FT NON_TER 1 1
 FT NON_TER 757 757
 SQ SEQUENCE 757 AA; 83859 MW; E32D6A1E6152F4F6 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 757;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
|||||
Db 169 IETWILRHP 177

RESULT 26
Q51CUG_9FLAV PRELIMINARY; PRT; 763 AA.
ID Q51CUG_9FLAV PRELIMINARY; PRT; 763 AA.
AC Q51CUG_9FLAV PRELIMINARY; PRT; 763 AA.
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Polypeptide (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxID=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RR1811;
RA Cruz A.C.R., Vasconcelos P.F.C., Ferreira A.P., Vasconcelos H.B.,
RA Jabor A.V., Travassos da Rosa E.S., Gallier R.,
RT "Genetic characterization of Dengue virus 2 and 3 isolated from
RT Brazil";
RL Submitted (0CT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY778961; AAW51132.1; -; Genomic_RNA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0019058; P:viral infectious cycle; IEA.
DR InterPro: IPR001122; Flavi_capsidC.
DR InterPro: IPR01999; Flavi_glycoE_cen.
DR InterPro: IPR000069; Flavi_M.
DR InterPro: IPR001157; Flavi_NS1.
DR InterPro: IPR002535; Flavi_propep.
DR InterPro: IPR000336; Flv_glyc_1g-like.
DR InterPro: IPR01998; Viral_glycoE_cen.
DR Pfam: PF01003; Flavi_capsid; 1.
DR Pfam: PF00869; Flavi_glycoprot; 1.
DR Pfam: PF02832; Flavi_glycop_C; 1.
DR Pfam: PF01004; Flavi_M; 1.
DR Pfam: PF00948; Flavi_NS1; 1.
DR Pfam: PF01570; Flavi_propep; 1.
DR ProDom: PD001556; Flavi_glycoprote; 1.
DR ProDom: PD001496; Flavi_NS1; 1.
KW Polypeptid.
FT NON_TER 1 763
SQ SEQUENCE 763 AA; 84631 MW; 0511E7D900193EB4 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 763;
Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
|||||
Db 162 IETWILRHP 170

RESULT 27
Q66398_9FLAV PRELIMINARY; PRT; 775 AA.
ID Q66398_9FLAV PRELIMINARY; PRT; 775 AA.
AC Q66398;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polypeptide (Fragment).
GN Name=C-PM-N-E;
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxID=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mexican;
RX MEDLINE=97042288; Pubmed=8887488;
RA Sanchez I.J., Ruiz B.H.;
RT "A single nucleotide change in the E protein gene of dengue virus 2
RT Mexican strain affects neurovirulence in mice";
RL J. Gen. Virol. 77:2541-2545 (1996).
DR EMBL: L04561; AAB42180.1; -; Genomic_RNA.
DR PIR: A48644; A48644.
DR HSP: Q88653; 10KE.
DR SMR: Q66398; 22-99, 281-674.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0019058; P:viral infectious cycle; IEA.
DR InterPro: IPR001122; Flavi_capsidC.
DR InterPro: IPR01999; Flavi_glycoE_cen.
DR InterPro: IPR000069; Flavi_M.
DR InterPro: IPR002535; Flavi_propep.
DR InterPro: IPR000336; Flv_glyc_1g-like.
DR InterPro: IPR01998; Viral_glycoE_cen.
DR Pfam: PF01003; Flavi_capsid; 1.
DR Pfam: PF00869; Flavi_glycoprot; 1.
DR Pfam: PF02832; Flavi_glycop_C; 1.
DR Pfam: PF01004; Flavi_M; 1.
DR Pfam: PF01570; Flavi_propep; 1.
DR ProDom: PD001556; Flavi_glycoprote; 1.
KW Polypeptid.
FT NON_TER 775
SQ SEQUENCE 775 AA; 87002 MW; D724768451B23438 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 775;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9

Db 237 IETWILRHP 245

RESULT 28

080Y62_9FLAV

ID 080Y62_9FLAV PRELIMINARY;

PRT; 775 AA.

AC 080Y62; 21-100, 281-674.

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Polypeptide (Fragment).

OS Dengue virus type 2.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Flavivirus; Dengue virus group.

OX NCBI_taxid=11060;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=GD08/98;

RA Ren R.W., Fang M.Y., Tian X.D., Liu J.W., Jiang L.H., Lin L.H.,

RA Zhao W.Z.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF469176; AAL79018.1; -; Genomic_RNA.

DR HSSP; Q88653; 10KE.

DR SMR; 080Y62; 21-100, 281-674.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0019058; P:viral infectious cycle; IEA.

DR InterPro; IPR001122; Flavi_capsidC.

DR InterPro; IPR011999; Flavi_glycoC_cen.

DR InterPro; IPR000069; Flavi_M.

DR InterPro; IPR002535; Flavi_propep.

DR InterPro; IPR000336; Flv_glyc_1g-like.

DR pfam; PF01003; Flavi_capsid; 1.

DR pfam; PF00869; Flavi_glycoprot; 1.

DR pfam; PF02832; Flavi_glycop_C; 1.

DR pfam; PF01570; Flavi_M; 1.

DR pfam; PF01570; Flavi_propep; 1.

DR ProDom; PD001556; Flavi_glycoprote; 1.

KW Polypeptide.

FT NON_TER 1 1

FT NON_TER 775 775

SQ SEQUENCE 775 AA; 86090 MW; 64BE26A0BF96B2C CRC64;

Query Match 100.0%; Score 53; DB 2; Length 775;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9

Db 237 IETWILRHP 245

RESULT 29

080Y63_9FLAV

ID 080Y63_9FLAV PRELIMINARY; PRT; 775 AA.

AC 080Y63; 21-100, 281-674.

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Polypeptide (Fragment).

OS Dengue virus type 2.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Flavivirus; Dengue virus group.

OX NCBI_taxid=11060;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=GD24/93;

RA Ren R.W., Fang M.Y., Tian X.D., Liu J.W., Jiang L.H., Lin L.H.,

RA Zhao W.Z.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF469175; AAL79017.1; -; Genomic_RNA.

DR HSSP; Q88653; 10KE.

DR SMR; 080Y63; 21-100, 281-674.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0019058; P:viral infectious cycle; IEA.

DR InterPro; IPR001122; Flavi_capsidC.

DR InterPro; IPR011999; Flavi_glycoC_cen.

DR InterPro; IPR000069; Flavi_M.

DR InterPro; IPR002535; Flavi_propep.

DR InterPro; IPR000336; Flv_glyc_1g-like.

DR pfam; PF01003; Flavi_capsid; 1.

DR pfam; PF00869; Flavi_glycoprot; 1.

DR pfam; PF02832; Flavi_glycop_C; 1.

DR pfam; PF01570; Flavi_M; 1.

DR pfam; PF01570; Flavi_propep; 1.

DR ProDom; PD001556; Flavi_glycoprote; 1.

KW Polypeptide.

FT NON_TER 1 1

FT NON_TER 775 775

SQ SEQUENCE 775 AA; 86055 MW; B5718CA10EC675B0 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 775;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9

Db 237 IETWILRHP 245

RESULT 30

080Y07_9FLAV

ID 080Y07_9FLAV PRELIMINARY; PRT; 775 AA.

AC 080Y07;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Polypeptide (Fragment).

OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_taxid=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Mar3;
RX MEDLINE=21571640; PubMed=11714970;
RA Uzcategui N.Y., Camacho D., Comach G., Cuello de Uzcategui R.,
RA Holmes E.C., Gould E.A.;
RT "Molecular epidemiology of dengue type 2 virus in Venezuela: evidence
RT for in situ virus evolution and recombination."
RL J. Gen. Virol. 82:2945-2953(2001).
DR EMBL: AY044442; AAL00888.1; -: Genomic RNA.
DR HSRF; Q88653; 10KE.
DR SMR; Q8QY07; 21-100, 281-674.
DR CO; CO:0019028; C:viral capsid; IEA.
DR CO; CO:0019031; C:viral envelope; IEA.
DR CO; CO:0005198; F:structural molecule activity; IEA.
DR CO; CO:0019058; P:viral infectious cycle; IEA.
DR InterPro; IPR001122; Flavi_capsidC.
DR InterPro; IPR001122; Flavi_glycoC.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR002535; Flavi_propep.
DR InterPro; IPR000336; Flv_glycE_Ig-like.
DR InterPro; IPR011988; Viral_glycoC_cen.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycoprot; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
KW Polyprotein.
FT CHAIN 1 150 capsid protein.
FT CHAIN 151 280 premembrane/membrane protein.
FT CHAIN 281 >775 envelope protein.
FT NON_TER 775 775
SQ SEQUENCE 775 AA; 86195 MW; 4DB2FCBE4287558 CRC64;

Query Match 100.0%; Score 53; DB 2; Length 775;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LETWILRHP 9
DB 237 LETWILRHP 245

Search completed: January 30, 2006, 09:15:54
Job time : 163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 30, 2006, 09:07:47 ; Search time 39 Seconds

(without alignments)
22:204 Million cell updates/sec

Title: US-10-608-147-29

Perfect score: 53

Sequence: 1 LETWILRHP 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	166	2 S40144	premembrane protei
2	53	100.0	555	2 JQ1404	genome polyprotein
3	53	100.0	775	2 A48644	polyprotein - deng
4	53	100.0	3388	1 GNMVDP	genome polyprotein
5	53	100.0	3391	1 GNMV16	genome polyprotein
6	53	100.0	3391	1 GNMV26	genome polyprotein
7	53	100.0	3391	1 GNMV2A	genome polyprotein
8	53	100.0	3391	2 J50219	polyprotein - deng
9	50	94.3	166	2 S09223	membrane protein -
10	50	94.3	166	2 S09225	membrane protein -
11	50	94.3	1127	1 GNMVD2	genome polyprotein
12	47	88.7	555	2 JQ1405	genome polyprotein
13	47	88.7	665	2 PS0043	genome polyprotein

[illegible]

128	33	62.3	203	2	A12445	hypothetical prote
129	33	62.3	216	2	G82532	outer membrane lip
130	33	62.3	226	2	E82677	conserved hypothet
131	33	62.3	262	2	F70790	probable hydrolase
132	33	62.3	264	2	F70790	probable hydrolase
133	33	62.3	272	2	C87711	hydrolase, alpha/b
134	33	62.3	274	2	S64523	translation elonga
135	33	62.3	290	2	E85709	unknown protein en
136	33	62.3	298	2	T20044	hypothetical prote
137	33	62.3	304	2	G85714	hypothetical prote
138	33	62.3	305	2	AH1154	oxidoreductase hom
139	33	62.3	305	2	AC1513	oxidoreductase hom
140	33	62.3	310	2	T35417	probable beta-lact
141	33	62.3	330	2	T30981	hypothetical prote
142	33	62.3	343	2	H95879	probable sugar ABC
143	33	62.3	365	1	A44764	choistamate mutase
144	33	62.3	365	2	G83250	choistamate mutase
145	33	62.3	447	2	F81678	GTP-binding protei
146	33	62.3	455	2	F91098	probable oxidoredu
147	33	62.3	455	2	A85944	hypothetical prote
148	33	62.3	456	2	S61170	BCS1 protein proteu
149	33	62.3	460	2	B85079	hypothetical prote
150	33	62.3	466	2	A64754	probable integrase

ALIGNMENTS

```

RESULT 1
S40144
premembrane protein - dengue virus type 2
C:Species: dengue virus type 2
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 31-Dec-2004
C:Accession: S40144
R:Shiu, S.Y.W.
submitted to the EMBL Data Library, May 1993
A:Reference number: S40144
A:Accession: S40144
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-166 <SH1>
NID:g437772; P1DN:CAA1363.1; PID:g939865
C:Superfamily: Hepatitis C virus genome polypeptide

Query Match          100.0%; Score 53; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
    | | | | | | | |
Db 123 IETWILRHP 131

RESULT 2
JQ1404
genome polypeptide - dengue virus type 2 (strain TH-36) (fragment)

N:Contains: envelope protein E; membrane-associated protein M; nonstructural
protein NS1
C:Species: dengue virus type 2
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: JQ1404
R:Shiu, S.Y.W.; Jiang, W.R.; Porterfield, J.S.; Gould, E.A.
J. Gen. Virol. 73, 207-212, 1992
A:Title: Envelope protein sequences of dengue virus isolates TH-36 and TH-Sman,
and identification of a type-specific genetic marker for dengue and tick-borne
flaviviruses.
A:Reference number: JQ1404; WUID:92113574; PMID:1339466
A:Accession: JQ1404
A:Molecule type: genomic RNA
A:Residues: 1-555 <SH1>
A:Cross-references: UNIPROT: P29984; UNIPARC:UP10000131DF8; GB:ID:0514;
DBJ:J01074; NID:g221248; P1DN:BA401389.1; PID:g221249
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: envelope protein; glycoprotein; nonstructural protein; polypeptide;
transmembrane protein
F:1-49/Product: membrane-associated protein M (fragment) #status predicted <END>
F:37-93/Domain: transmembrane #status predicted <TM1>
F:50-544/Product: envelope protein E #status predicted <ENV>
F:496-512/Domain: transmembrane #status predicted <TM2>
F:526-542/Domain: transmembrane #status predicted <TM3>
F:545-555/Product: nonstructural protein NS1 (fragment) #status predicted <NON>
F:116,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

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Query Match          100.0%; Score 53; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
    | | | | | | | |
Db 6 IETWILRHP 14

RESULT 3
A48644
polypeptide - dengue virus type 2 (strain Mexican) (fragment)
C:Species: dengue virus type 2
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 31-Dec-2004
C:Accession: A48644
R:Ruiz, B.H.; Sanchez, I.; Ortega, G.J.; Lopez, I.; Ortiz-Ortiz, L.
submitted to Genbank, October 1992
A:Description: Nucleotide sequence and deduced amino-acid sequence of the
structural proteins of Dengue type 2 virus Mexican genotype.
A:Reference number: A48644
A:Accession: A48644
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-775 <RUI>
A:Cross-references: UNIPROT: P06398; UNIPARC:UP100000EE45; GB:L04561;
NID:g323652; P1DN:ABA2180.1; PID:g554632
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: polypeptide

Query Match          100.0%; Score 53; DB 2; Length 775;

```

Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWLRHP 9
|||||
Db 237 IETWLRHP 245

RESULT 4

GNMWDP
genome polypeptide - dengue virus type 2 (strain PR159/S1)
N:Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS1; nonstructural protein NS2a; nonstructural protein NS2b; nonstructural protein NS3; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: dengue virus type 2
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 31-Dec-2004
C:Accession: A29972
R:Rahm, Y.S.; Galter, R.; Hunkapiller, T.; Dalrymple, J.M.; Strauss, J.H.; Strauss, E.G.
Virology 162, 167-180, 1988
A:Title: Nucleotide sequence of dengue 2 RNA and comparison of the encoded proteins with those of other flaviviruses.
A:Reference number: A29972; PMID:88101365; PMID:2827375
A:Accession: A29972
A:Molecule type: genomic RNA
A:Residues: 1-3388 <HAH>
A:Cross-references: UNIPARC:UP10000131DFB; GB:M19197; NID:9323654;
P1DN:AAA42962.1; PID:9323655
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; membrane protein; nonstructural protein; nucleotide binding; P-loop
F:211-280/Product: capsid protein #status predicted <CAP>
F:115-280/Product: membrane protein precursor #status predicted <MP>
F:115-205/Domain: nonterminal signal sequence #status predicted <SIG>
F:206-280/Product: membrane protein #status predicted <MP>
F:281-775/Product: envelope protein #status predicted <ENP>
F:776-1188/Product: nonstructural protein NS1 #status predicted <NS1>
F:1189-1345/Product: nonstructural protein NS2a #status predicted <NS2a>
F:1346-1474/Product: nonstructural protein NS2b #status predicted <NS2b>
F:1476-2090/Product: nonstructural protein NS3 #status predicted <NS3>
F:1668-1675/Region: nucleotide-binding motif A (P-loop)
F:1755-1760/Region: nucleotide-binding motif B
F:1759-1762/Region: DEAH motif
F:2091-2376/Product: nonstructural protein NS4a #status predicted <NS4a>
F:2377-2488/Product: nonstructural protein NS4b #status predicted <NS4b>
F:2489-3388/Product: nonstructural protein NS5 #status predicted <NS5>
F:183,347,433,905,982,1134,1174,1329,1369,2298,2302,2384,2454,2482,2641,2662,2701,2711/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 53; DB 1; Length 3388;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IETWLRHP 9
|||||
Db 237 IETWLRHP 245

RESULT 5

GNMW16
genome polypeptide - dengue virus type 2 (strain 16681)
N:Contains: capsid protein C; envelope protein E; membrane-associated protein M; nonstructural protein NS1; nonstructural protein NS2a; nonstructural protein NS2b; nonstructural protein NS3; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: dengue virus type 2
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 31-Dec-2004
C:Accession: A42451; A43966; A43763
R:Block, J.; McMilliam, S.M.; Butler, H.C.; Gibbs, A.J.; Wellner, G.; Herring, B.L.; Hensley, A.C.; Askov, J.G.; Yoksan, S.; Bhattacharjee, N.
Virology 187, 573-590, 1992
A:Title: Comparison of a dengue-2 virus and its candidate vaccine derivative: sequence relationships with the flaviviruses and other viruses.
A:Reference number: A42451; PMID:92188532; PMID:1312269
A:Accession: A42451
A:Molecule type: genomic RNA
A:Residues: 1-3391 <BLD>
A:Cross-references: UNIPROT:P29990; UNIPARC:UP10000131DF5; GB:M84727; GB:M85259;
NID:9323472; P1DN:AAA73185.1; PID:9323473
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein; nucleotide binding; P-loop; polypeptide; transmembrane protein
F:114-114/Product: capsid protein C #status predicted <CPC>
F:115-280/Product: membrane-associated protein M precursor #status predicted <MP>

F:115-205/Domain: nonterminal signal sequence #status predicted <SIG>
F:206-280/Product: membrane-associated protein M #status predicted <MP>
F:268-284/Domain: transmembrane #status predicted <TM>
F:281-775/Product: envelope protein E #status predicted <EPP>
F:727-743/Domain: transmembrane #status predicted <TM>
F:757-773/Domain: transmembrane #status predicted <TM>
F:776-1187/Product: nonstructural protein NS1 #status predicted <NS1>
F:1128-1345/Product: nonstructural protein NS2a #status predicted <NS2a>
F:1346-1474/Product: nonstructural protein NS2b #status predicted <NS2b>
F:1475-2093/Product: nonstructural protein NS3 #status predicted <NS3>
F:1668-1675/Region: nucleotide-binding motif A (P-loop)
F:1755-1760/Region: nucleotide-binding motif B
F:1759-1762/Region: DEAH motif
F:2094-2243/Product: nonstructural protein NS4a #status predicted <NS4a>
F:2244-2491/Product: nonstructural protein NS4b #status predicted <NS4b>
F:2492-3391/Product: nonstructural protein NS5 #status predicted <NS5>
F:183,347,433/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 53; DB 1; Length 3391;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IETWLRHP 9
|||||
Db 237 IETWLRHP 245

RESULT 6

GNMV26

genome polyprotein - dengue virus type 2 (strain 16681-PD/53)

N:contains: capsid protein C; envelope protein E; membrane-associated protein M; nonstructural protein NS1; nonstructural protein NS2a; nonstructural protein NS2b; nonstructural protein NS3; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5

C:Species: dengue virus type 2

C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 31-Dec-2004

C:Accession: B42451

R:Blot, J.; McWilliam, S.M.; Butler, H.C.; Gibbs, A.J.; Weiller, G.; Herring, B.L.; Hensley, A.C.; Aaskov, J.G.; Yoksan, S.; Bhamarepravati, N.

Virology 187, 573-590, 1992

A:Title: Comparison of a dengue-2 virus and its candidate vaccine derivative: sequence relationships with the flaviviruses and other viruses.

A:Reference number: A42451; PMID:92188532; PMID:1312269

A:Accession: B42451

A:Molecule type: genomic RNA

A:Residues: 1-3391 <BLO>

A:Cross-references: UNIPROT:P29991; UNIPARC:UP10000131DF6; GB:M65259

C:Superfamily: Hepatitis C virus genome polyprotein

C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein; nucleotide binding; P-loop; polypeptide; transmembrane protein

F:1-114/Product: capsid protein C #status predicted <CPC>

F:50-66/Domain: transmembrane #status predicted <TM1>

F:102-118/Domain: transmembrane #status predicted <TM2>

F:115-280/Product: membrane-associated protein M precursor #status predicted <MP>

F:115-205/Domain: nonterminal signal sequence #status predicted <SIG>

F:206-280/Product: membrane-associated protein M #status predicted <MMP>

F:268-284/Domain: transmembrane #status predicted <TM3>

F:281-773/Product: envelope protein E #status predicted <EPE>

F:727-743/Domain: transmembrane #status predicted <TM4>

F:757-773/Domain: transmembrane #status predicted <TM5>

F:776-1127/Product: nonstructural protein NS1 #status predicted <NS1>

F:1128-1345/Product: nonstructural protein NS2a #status predicted <NS2a>

F:1158-1174/Domain: transmembrane #status predicted <TM6>

F:1272-1288/Domain: transmembrane #status predicted <TM7>

F:1294-1310/Domain: transmembrane #status predicted <TM8>

F:1346-1474/Product: nonstructural protein NS2b #status predicted <NS2b>

F:1351-1367/Domain: transmembrane #status predicted <TM9>

F:1373-1389/Domain: transmembrane #status predicted <TMa>

F:1448-1464/Domain: transmembrane #status predicted <TMb>

F:1475-2093/Product: nonstructural protein NS3 #status predicted <NS3>

F:1668-1675/Region: nucleotide-binding motif A (P-loop)

F:1755-1760/Region: nucleotide-binding motif B

F:1759-1762/Region: DEAH motif

F:2094-2243/Product: nonstructural protein NS4a #status predicted <NS4a>

F:2148-2164/Domain: transmembrane #status predicted <TMc>

F:2174-2190/Domain: transmembrane #status predicted <TMd>

F:2197-2213/Domain: transmembrane #status predicted <TMe>

F:2227-2243/Domain: transmembrane #status predicted <TMf>

F:2244-2491/Product: nonstructural protein NS4b #status predicted <NS4b>

F:2352-2368/Domain: transmembrane #status predicted <TMg>

F:2411-2427/Domain: transmembrane #status predicted <TMh>

F:2492-3391/Product: nonstructural protein NS5 #status predicted <NS5>

F:183,347,433,905,982,1134,1174,1329,2301,2305,2346,2387,2457,2485,2644,2665,2704,2714/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 53; DB 1; Length 3391;

Best Local Similarity 100.0%; Pred. No. 0.81;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWLRHP 9

Db 237 IETWLRHP 245

RESULT 7

GNMV2A

genome polyprotein - dengue virus type 2 (strain Jamaica)

N:contains: capsid protein C; envelope protein E; membrane-associated protein M; nonstructural protein NS1; nonstructural protein NS2a; nonstructural protein NS2b; nonstructural protein NS3; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5

C:Species: dengue virus type 2

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 31-Dec-2004

C:Accession: A94346; A94378; A25613; A29199

R:Deubel, V.; Kinney, R.M.; Trent, D.W.

Virology 155, 365-377, 1986

A:Title: Nucleotide sequence and deduced amino acid sequence of the structural proteins of dengue type 2 virus, Jamaica genotype.

A:Reference number: A94346; PMID:87071658; PMID:3024394

A:Accession: A94346

A:Molecule type: genomic RNA

A:Residues: 1-791 <DE1>

A:Cross-references: UNIPROT:P07564; UNIPARC:UP100001710B8; GB:M15975

R:Deubel, V.; Kinney, R.M.; Trent, D.W.

Virology 165, 234-244, 1988

A:Title: Nucleotide sequence and deduced amino acid sequence of the nonstructural proteins of dengue type 2 virus, Jamaica genotype: comparative analysis of the full-length genome.

A:Reference number: A94378; PMID:88265864; PMID:3388770

A:Accession: A94378

A:Molecule type: genomic RNA

A:Residues: 792-3391 <DE2>

A:Cross-references: UNIPARC:UP10000174A05; GB:M20558

C:Superfamily: Hepatitis C virus genome polyprotein

C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein; nucleotide binding; P-loop; polypeptide; transmembrane protein

F:2-114/Product: capsid protein C #status predicted <CPC>

F:43-59/Domain: transmembrane #status predicted <TM1>

F:101-111/Domain: transmembrane #status predicted <TM2>

F:115-280/Product: membrane-associated protein M precursor #status predicted <MP>

F:115-205/Domain: nonterminal signal sequence #status predicted <SIG>

F:206-280/Product: membrane-associated protein M #status predicted <MMP>

F:268-284/Domain: transmembrane #status predicted <TM3>

F:281-775/Product: envelope protein E #status predicted <EPE>

F:727-743/Domain: transmembrane #status predicted <TM4>

F:757-773/Domain: transmembrane #status predicted <TM5>

F:776-1127/Product: nonstructural protein NS1 #status predicted <NS1>

F:1128-1345/Product: nonstructural protein NS2a #status predicted <NS2a>

F:1346-1474/Product: nonstructural protein NS2b #status predicted <NS2b>
F:1745-2093/Product: nonstructural protein NS3 #status predicted <NS3>
F:1668-1675/Region: nucleotide-binding motif A (P-loop)
F:1755-1760/Region: nucleotide-binding motif B
F:1759-1762/Region: DEAH motif
F:2094-2243/Product: nonstructural protein NS4a #status predicted <NS4a>
F:2244-2491/Product: nonstructural protein NS4b #status predicted <NS4b>
F:2492-3391/Product: nonstructural protein NS5 #status predicted <NS5>
F:183,347,433/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 53; DB 1; Length 3391;
Best Local Similarity 100.0%; Pred. No. 0.81;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
|||||
Db 237 IETWILRHP 245

RESULT 8

polyprotein - dengue virus type 2 (strain New Guinea-C)
N:Contains: capsid protein; envelope protein; membrane glycoprotein;
nonstructural protein NS1; nonstructural protein NS2A; nonstructural protein
NS2B; nonstructural protein NS3; nonstructural protein NS4A; nonstructural
protein NS4B; nonstructural protein NS5

C:Species: dengue virus type 2

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004

C:Accession: J50219; A28646

R:Irle, K.; Mohan, P.M.; Sasaguri, Y.; Putnak, R.; Padmanabhan, R.

Gene 75, 197-211, 1989

A:Title: Sequence analysis of cloned dengue virus type 2 genome (New Guinea-C strain).

A:Reference number: J50219; MUID:89232751; PMID:2714651

A:Accession: J50219

A:Molecule type: genomic RNA

A:Residues: 1-3391 <IR>

A:Cross-References: UNIPROT:Q9Q4T2; UNIPROT:Q9WLZ4; UNIPROT:Q9WDN6;

UNIPROT:Q9JBD4; UNIPROT:Q9IU94; UNIPROT:Q9WLZ5; UNIPROT:Q9JBD1; UNIPROT:Q9JBD6;

UNIPROT:Q9WDA4; UNIPROT:Q9WDA2; UNIPROT:Q9JBD5; UNIPROT:Q9JBD8;

UNIPROT:Q9WDA7; UNIPROT:Q92753; UNIPROT:Q9JBD3; UNIPROT:Q9YKL3;

UNIPROT:Q9WZ77; UNIPROT:Q92754; UNIPROT:Q9E7P0; UNIPROT:Q91H74; UNIPROT:Q9Q4T1;

UNIPROT:Q9JBE0; UNIPROT:Q9W813; UNIPROT:Q9JBD7; UNIPROT:Q9WDA3; UNIPROT:Q11875;

UNIPROT:Q92835; UNIPROT:Q09234

R:Putnak, J.R.; Charles, P.C.; Padmanabhan, R.; Irle, K.; Hohe, C.H.; Burke,

D.S.

Virology 163, 93-103, 1988

A:Title: Functional and antigenic domains of the dengue-2 virus nonstructural

glycoprotein NS-1.

A:Reference number: A28646; MUID:88160069; PMID:2964755

A:Accession: A28646

A:Molecule type: genomic RNA

A:Residues: 749-1227 <PU>

A:Cross-References: UNIPARC:UPI0000178549

C:Keywords: ATP; envelope protein; glycoprotein; nonstructural protein;

nucleotide binding; P-loop; polypeptide; transmembrane protein

F:2-114/Product: capsid protein #status predicted <CAP>

F:115-280/Product: membrane glycoprotein #status predicted <MEM>
F:115-205/Domain: nonterminal signal sequence #status predicted <SIG>
F:206-280/Product: membrane glycoprotein #status predicted <MEB>
F:281-775/Product: envelope protein #status predicted <ENV>
F:755-775/Domain: transmembrane #status predicted <TM1>
F:776-1127/Product: nonstructural protein NS1 #status experimental <NS1>
F:1128-1345/Product: nonstructural protein NS2A #status predicted <NS2>
F:1135-1146/Domain: transmembrane #status predicted <TM2>
F:1158-1173/Domain: transmembrane #status predicted <TM3>

F:1346-1475/Product: nonstructural protein NS2B #status predicted <NSB>

F:1476-2093/Product: nonstructural protein NS3 #status experimental <NS3>

F:1668-1675/Region: nucleotide-binding motif A (P-loop)

F:1755-1760/Region: nucleotide-binding motif B

F:1759-1762/Region: DEAH motif

F:2094-2379/Product: nonstructural protein NS4A #status predicted <NS4>

F:2380-2491/Product: nonstructural protein NS4B #status predicted <NS4B>

F:2492-3391/Product: nonstructural protein NS5 #status experimental <NS5>

F:183,905,982,2305,2457,2704/Binding site: carboxylate (Asn) (covalent) #status

experimental

F:347,433,1134,1174,2301,2485,2665,2714/Binding site: carboxylate (Asn)

(covalent) #status predicted

Query Match 100.0%; Score 53; DB 2; Length 3391;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
|||||
Db 237 IETWILRHP 245

Search completed: January 30, 2006, 09:16:46
Job time : 43 secs

OM protein - protein search, using sw model

Run on: January 30, 2006, 09:13:08 ; Search time 7 Seconds
(without alignments)
13.923 Million cell updates/sec

Title: US-10-608-147-29

Perfect score: 53

Sequence: 1 IETWLRHP 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 150 summaries

Database :
1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:.*
2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:.*
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:.*
4: /cgn2_6/prodata/1/pubpaa/PC7_NEW_PUB.pep:.*
5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:.*
6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:.*
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep:.*
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	71.7	248	7	US-11-060-295-4
2	38	71.7	684	6	US-10-714-781A-55
3	38	71.7	684	6	US-10-714-781A-57
4	38	71.7	684	6	US-10-714-781A-61
5	38	71.7	686	6	US-10-714-781A-59
6	38	71.7	3433	6	US-10-714-781A-67
7	36	67.9	516	6	US-10-508-263-26
8	34	64.2	207	6	US-10-467-657-4974
9	34	64.2	248	7	US-11-054-515-1960

10	34	64.2	444	7	US-11-112-882-15	Sequence 15, Appl
11	33	62.3	562	6	US-10-508-263-24	Sequence 24, Appl
12	33	62.3	777	6	US-10-821-234-1658	Sequence 1658, Ap
13	32	60.4	133	6	US-10-746-909-6	Sequence 6, Appl1
14	32	60.4	311	6	US-10-793-626-1260	Sequence 1260, Ap
15	32	60.4	390	6	US-10-525-710-16	Sequence 16, Appl
16	32	60.4	702	6	US-10-510-386-214	Sequence 214, App
17	32	60.4	1137	6	US-10-499-715-4	Sequence 4, Appl1
18	32	60.4	2897	6	US-10-499-715-2	Sequence 2, Appl1
19	31	58.5	149	7	US-11-052-554A-314	Sequence 314, App
20	31	58.5	194	7	US-11-194-246-318	Sequence 318, App
21	31	58.5	201	6	US-10-467-657-5346	Sequence 5346, Ap
22	31	58.5	446	7	US-11-112-882-68	Sequence 68, Appl
23	31	58.5	508	6	US-10-467-657-6928	Sequence 6928, Ap
24	31	58.5	532	6	US-10-063-703-72	Sequence 72, Appl
25	31	58.5	532	7	US-11-102-240-72	Sequence 72, Appl
26	31	58.5	559	6	US-10-521-162-4	Sequence 4, Appl1
27	31	58.5	629	6	US-10-467-657-1130	Sequence 1130, Ap
28	31	58.5	712	6	US-10-521-162-12	Sequence 12, Appl
29	31	58.5	1433	7	US-11-094-519A-40	Sequence 40, Appl
30	30	56.6	76	7	US-11-128-900-85	Sequence 85, Appl
31	30	56.6	80	6	US-10-714-887-384	Sequence 384, App
32	30	56.6	99	7	US-11-054-669-36	Sequence 36, Appl
33	30	56.6	99	7	US-11-054-669-39	Sequence 39, Appl
34	30	56.6	99	7	US-11-084-554-50	Sequence 50, Appl
35	30	56.6	99	7	US-11-004-590-43	Sequence 43, Appl
36	30	56.6	144	6	US-10-453-372-72	Sequence 72, Appl
37	30	56.6	172	7	US-11-128-900-7	Sequence 7, Appl1
38	30	56.6	172	7	US-11-128-900-86	Sequence 86, Appl
39	30	56.6	210	6	US-10-793-626-524	Sequence 524, App
40	30	56.6	252	7	US-11-054-515-1994	Sequence 1994, Ap
41	30	56.6	253	7	US-11-054-515-1619	Sequence 1619, Ap
42	30	56.6	297	6	US-10-453-372-70	Sequence 70, Appl
43	30	56.6	359	6	US-10-793-626-2454	Sequence 2454, Ap
44	30	56.6	364	7	US-11-067-884-2	Sequence 2, Appl1
45	30	56.6	382	6	US-10-858-730-23	Sequence 23, Appl1
46	30	56.6	382	6	US-10-525-674-4	Sequence 4, Appl1
47	30	56.6	469	6	US-10-467-657-6054	Sequence 6054, Ap
48	30	56.6	550	6	US-10-453-372-76	Sequence 76, Appl
49	30	56.6	575	6	US-10-453-372-78	Sequence 78, Appl
50	30	56.6	578	6	US-10-453-372-66	Sequence 66, Appl
51	30	56.6	578	6	US-10-453-372-80	Sequence 80, Appl
52	30	56.6	1068	6	US-10-467-657-2904	Sequence 2904, Ap
53	29.5	55.7	809	6	US-10-467-657-1106	Sequence 1106, Ap
54	29.5	55.7	810	7	US-11-052-554A-245	Sequence 245, App
55	29	54.7	144	6	US-10-793-626-1640	Sequence 1640, Ap
56	29	54.7	144	6	US-10-793-626-1958	Sequence 1958, Ap
57	29	54.7	179	7	US-11-010-239-6	Sequence 6, Appl1
58	29	54.7	200	7	US-11-127-622-4	Sequence 4, Appl1
59	29	54.7	234	6	US-10-063-703-14	Sequence 14, Appl
60	29	54.7	234	7	US-11-102-240-14	Sequence 14, Appl
61	29	54.7	255	6	US-10-793-626-914	Sequence 914, App
62	29	54.7	255	6	US-10-793-626-2620	Sequence 2620, Ap
63	29	54.7	256	7	US-11-054-515-1745	Sequence 1745, Ap
64	29	54.7	276	7	US-11-054-281-85	Sequence 85, Appl
65	29	54.7	277	7	US-11-054-281-84	Sequence 84, Appl
66	29	54.7	305	5	US-09-978-360A-446	Sequence 446, App

67 29 54.7 327 7 US-11-152-811-5 Sequence 5, Appl1
68 29 54.7 338 6 US-10-632-150-12 Sequence 12, Appl
69 29 54.7 338 7 US-11-073-457-12 Sequence 12, Appl
70 29 54.7 338 7 US-11-073-460-12 Sequence 12, Appl
71 29 54.7 377 6 US-10-467-657-680 Sequence 680, App
72 29 54.7 377 6 US-10-467-657-4946 Sequence 4946, Ap
73 29 54.7 428 7 US-11-127-622-2 Sequence 2, Appl1
74 29 54.7 428 7 US-11-127-877-73 Sequence 73, Appl
75 29 54.7 434 6 US-10-467-657-3230 Sequence 3230, Ap
76 29 54.7 444 7 US-11-112-882-21 Sequence 21, Appl
77 29 54.7 449 7 US-11-112-882-71 Sequence 71, Appl
78 29 54.7 522 6 US-10-131-826A-450 Sequence 450, Appl
79 29 54.7 524 6 US-10-793-626-3090 Sequence 3090, Ap
80 29 54.7 538 6 US-10-793-626-3134 Sequence 3134, Ap
81 29 54.7 539 7 US-11-024-959-436 Sequence 436, App
82 29 54.7 564 6 US-10-793-626-3220 Sequence 3220, Ap
83 29 54.7 573 6 US-10-525-710-36 Sequence 36, Appl
84 29 54.7 581 7 US-11-045-802-30 Sequence 30, Appl
85 29 54.7 584 7 US-11-045-802-31 Sequence 31, Appl
86 29 54.7 648 7 US-11-127-877-72 Sequence 72, Appl
87 29 54.7 692 7 US-11-103-957-29 Sequence 29, Appl
88 29 54.7 782 6 US-10-995-561-861 Sequence 861, App
89 29 54.7 847 6 US-10-995-561-863 Sequence 863, App
90 29 54.7 847 6 US-10-995-561-865 Sequence 865, App
91 29 54.7 905 7 US-11-124-368A-307 Sequence 307, App
92 29 54.7 1148 7 US-11-110-082-29 Sequence 29, Appl
93 29 54.7 1149 7 US-11-110-082-30 Sequence 30, Appl
94 29 54.7 1172 7 US-11-186-284-203 Sequence 203, App
95 29 54.7 3748 7 US-11-132-686-8 Sequence 8, Appl1
96 29 54.7 3749 7 US-11-132-686-6 Sequence 6, Appl1
97 29 54.7 3749 7 US-11-132-686-12 Sequence 12, Appl
98 29 54.7 3912 7 US-11-132-686-7 Sequence 7, Appl1
99 29 54.7 3913 7 US-11-132-686-5 Sequence 5, Appl1
100 29 54.7 3913 7 US-11-132-686-9 Sequence 9, Appl1
101 28 52.8 12 6 US-10-929-988-166 Sequence 166, App
102 28 52.8 18 6 US-10-929-988-192 Sequence 192, App
103 28 52.8 65 7 US-11-045-802-37 Sequence 37, Appl
104 28 52.8 131 7 US-11-124-368A-326 Sequence 326, App
105 28 52.8 180 7 US-11-165-697-47 Sequence 47, Appl
106 28 52.8 198 6 US-10-467-657-4664 Sequence 4664, Ap
107 28 52.8 254 6 US-10-510-386-146 Sequence 146, App
108 28 52.8 254 6 US-10-510-386-178 Sequence 178, App
109 28 52.8 312 6 US-10-495-597-6 Sequence 6, Appl1
110 28 52.8 314 7 US-11-156-094-196 Sequence 196, App
111 28 52.8 321 6 US-10-467-657-216 Sequence 216, App
112 28 52.8 342 7 US-11-156-084-309 Sequence 7912, Ap
113 28 52.8 364 6 US-10-793-626-3076 Sequence 3076, Ap
114 28 52.8 395 6 US-10-858-730-218 Sequence 218, App
115 28 52.8 407 7 US-11-092-140-4 Sequence 4, Appl1
116 28 52.8 444 7 US-11-112-882-22 Sequence 22, Appl
117 28 52.8 449 6 US-10-878-556A-57 Sequence 57, Appl
118 28 52.8 449 7 US-11-112-882-70 Sequence 70, Appl
119 28 52.8 466 6 US-10-957-569-28 Sequence 28, Appl
120 28 52.8 480 6 US-10-521-162-40 Sequence 40, Appl
121 28 52.8 487 7 US-11-024-959-495 Sequence 495, App
122 28 52.8 529 7 US-11-033-039-487 Sequence 487, App
123 28 52.8 529 7 US-11-033-039-487

124 28 52.8 529 7 US-11-155-288-1 Sequence 1, Appl1
125 28 52.8 533 6 US-10-467-657-2868 Sequence 2868, Ap
126 28 52.8 548 6 US-10-467-657-7704 Sequence 7704, Ap
127 28 52.8 548 6 US-10-053-877-320 Sequence 320, App
128 28 52.8 564 6 US-10-517-939-288 Sequence 288, App
129 28 52.8 565 6 US-10-055-877-228 Sequence 228, App
130 28 52.8 579 7 US-11-045-802-32 Sequence 32, Appl
131 28 52.8 579 7 US-11-045-802-33 Sequence 33, Appl
132 28 52.8 613 6 US-10-055-877-227 Sequence 227, App
133 28 52.8 613 6 US-10-055-877-117 Sequence 117, App
134 28 52.8 675 6 US-10-055-877-317 Sequence 317, App
135 28 52.8 675 6 US-10-055-877-318 Sequence 318, App
136 28 52.8 702 7 US-11-043-788-371 Sequence 371, App
137 28 52.8 727 7 US-11-043-788-367 Sequence 367, App
138 28 52.8 727 7 US-11-043-788-368 Sequence 368, App
139 28 52.8 729 7 US-11-043-788-373 Sequence 373, App
140 28 52.8 736 7 US-11-043-788-372 Sequence 372, App
141 28 52.8 774 7 US-11-043-788-370 Sequence 370, App
142 28 52.8 843 7 US-11-129-104-89 Sequence 89, Appl
143 28 52.8 862 6 US-10-645-441-15 Sequence 15, Appl
144 28 52.8 882 6 US-10-725-475-7 Sequence 7, Appl1
145 28 52.8 892 7 US-11-050-804-6 Sequence 6, Appl1
146 28 52.8 909 7 US-11-186-284-2 Sequence 2, Appl1
147 28 52.8 913 6 US-10-821-234-1040 Sequence 1040, Ap
148 28 52.8 1170 6 US-10-831-997-2 Sequence 2, Appl1
149 28 52.8 1170 6 US-10-995-561-594 Sequence 594, App
150 28 52.8 1170 6 US-10-995-561-595 Sequence 595, App

Search completed: January 30, 2006, 09:19:11
Job time : 7 secs

OM protein - protein search, using sw model

Run on: January 30, 2006, 09:10:38 : Search time 61 seconds
(without alignments)
61.647 Million cell updates/sec

Title: US-10-608-147-29

Perfect score: 53

Sequence: 1 LETWILRHP 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : Published Applications AA>Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Query Length	DB ID	Description
1	53	100.0	9	US-10-608-147-29
2	53	100.0	21	US-10-608-147-36
3	53	100.0	32	US-10-608-147-35
4	53	100.0	39	US-10-608-029-23
5	53	100.0	40	US-10-311-213-3
6	53	100.0	40	US-10-608-029-25
7	53	100.0	40	US-10-608-147-31
8	53	100.0	48	US-10-311-213-32
9	53	100.0	167	US-10-375-932-122
10	53	100.0	171	US-10-375-932-118
11	53	100.0	171	US-10-375-932-121

12	53	100.0	675	4	US-10-375-932-143	Sequence 143, App
13	53	100.0	675	4	US-10-375-932-237	Sequence 237, App
14	53	100.0	675	4	US-10-375-932-237	Sequence 251, App
15	53	100.0	675	4	US-10-375-932-238	Sequence 253, App
16	53	100.0	677	4	US-10-375-932-142	Sequence 238, App
17	53	100.0	681	4	US-10-375-932-142	Sequence 142, App
18	53	100.0	681	4	US-10-375-932-228	Sequence 228, App
19	53	100.0	685	5	US-10-500-796A-43	Sequence 43, App1
20	53	100.0	685	5	US-10-500-796A-45	Sequence 45, App1
21	53	100.0	685	5	US-10-500-796A-47	Sequence 47, App1
22	53	100.0	1127	4	US-10-247-960-3	Sequence 3, App1
23	53	100.0	3388	5	US-10-719-547-17	Sequence 17, App1
24	53	100.0	3391	5	US-10-719-547-21	Sequence 21, App1
25	53	100.0	3391	5	US-10-871-775-31	Sequence 31, App1
26	49	92.5	39	5	US-10-608-029-29	Sequence 29, App1
27	49	92.5	48	5	US-10-608-029-35	Sequence 35, App1
28	48	90.6	40	3	US-09-881-710-29	Sequence 29, App1
29	48	90.6	40	4	US-10-634-895-29	Sequence 29, App1
30	47	88.7	9	5	US-10-608-147-40	Sequence 40, App1
31	47	88.7	35	4	US-10-311-213-13	Sequence 13, App1
32	47	88.7	40	3	US-09-881-710-28	Sequence 28, App1
33	47	88.7	40	4	US-10-634-895-28	Sequence 28, App1
34	47	88.7	40	4	US-10-311-213-1	Sequence 1, App1
35	47	88.7	40	4	US-10-311-213-20	Sequence 20, App1
36	47	88.7	40	5	US-10-608-147-38	Sequence 38, App1
37	47	88.7	47	4	US-10-311-213-9	Sequence 9, App1
38	47	88.7	76	3	US-09-881-710-1	Sequence 1, App1
39	47	88.7	76	4	US-10-634-895-1	Sequence 1, App1
40	47	88.7	167	4	US-10-375-932-117	Sequence 117, App1
41	47	88.7	167	4	US-10-375-932-119	Sequence 119, App1
42	47	88.7	167	4	US-10-375-932-123	Sequence 123, App1
43	47	88.7	167	4	US-10-375-932-125	Sequence 125, App1
44	47	88.7	167	4	US-10-375-932-126	Sequence 126, App1
45	47	88.7	661	5	US-10-701-122-51	Sequence 51, App1
46	47	88.7	675	4	US-10-375-932-144	Sequence 144, App1
47	47	88.7	675	4	US-10-375-932-146	Sequence 146, App1
48	47	88.7	675	4	US-10-375-932-148	Sequence 148, App1
49	47	88.7	675	4	US-10-375-932-229	Sequence 229, App1
50	47	88.7	675	4	US-10-375-932-236	Sequence 236, App1
51	47	88.7	675	4	US-10-375-932-239	Sequence 239, App1
52	47	88.7	675	4	US-10-375-932-240	Sequence 240, App1
53	47	88.7	675	4	US-10-375-932-241	Sequence 241, App1
54	47	88.7	675	4	US-10-375-932-243	Sequence 243, App1
55	47	88.7	675	4	US-10-375-932-245	Sequence 245, App1
56	47	88.7	675	4	US-10-375-932-246	Sequence 246, App1
57	47	88.7	676	4	US-10-375-932-249	Sequence 249, App1
58	47	88.7	677	4	US-10-375-932-244	Sequence 244, App1
59	47	88.7	677	4	US-10-375-932-140	Sequence 140, App1
60	47	88.7	677	4	US-10-375-932-147	Sequence 147, App1
61	47	88.7	677	4	US-10-375-932-227	Sequence 227, App1
62	47	88.7	677	4	US-10-375-932-242	Sequence 242, App1
63	47	88.7	681	4	US-10-375-932-247	Sequence 247, App1
64	47	88.7	3390	5	US-10-719-547-22	Sequence 22, App1
65	47	88.7	3392	5	US-10-719-547-20	Sequence 20, App1
66	44	83.0	362	4	US-10-424-599-277008	Sequence 277008, App1
67	44	83.0	364	4	US-10-425-114-54836	Sequence 54836, App1
68	44	83.0	611	4	US-10-282-122A-50813	Sequence 50813, App1

69	44	83.0	8601	5	US-10-496-377-7	Sequence 7, Appl
70	43	81.1	3390	5	US-10-871-775-33	Sequence 33, Appl
71	41	77.4	167	4	US-10-375-932-120	Sequence 120, App
72	41	77.4	167	4	US-10-375-932-124	Sequence 124, App
73	41	77.4	675	4	US-10-375-932-139	Sequence 139, App
74	41	77.4	675	4	US-10-375-932-145	Sequence 145, App
75	41	77.4	675	4	US-10-375-932-145	Sequence 250, App
76	41	77.4	675	4	US-10-375-932-248	Sequence 252, App
77	41	77.4	676	4	US-10-375-932-141	Sequence 141, App
78	41	77.4	677	4	US-10-375-932-230	Sequence 230, App
79	41	77.4	677	4	US-10-375-932-343	Sequence 343, App
80	41	77.4	677	4	US-10-375-932-345	Sequence 345, App
81	41	77.4	678	4	US-10-375-932-348	Sequence 249, App
82	41	77.4	3387	5	US-10-719-547-13	Sequence 13, Appl
83	41	77.4	3387	5	US-10-719-547-15	Sequence 13, Appl
84	41	77.4	3387	5	US-10-719-547-19	Sequence 19, Appl
85	40	75.5	39	3	US-09-881-710-12	Sequence 12, Appl
86	40	75.5	39	3	US-09-881-710-30	Sequence 30, Appl
87	40	75.5	39	4	US-10-634-895-12	Sequence 12, Appl
88	40	75.5	39	4	US-10-634-895-30	Sequence 30, Appl
89	40	75.5	149	3	US-09-738-626-6297	Sequence 6297, Ap
90	40	75.5	149	3	US-10-424-599-279000	Sequence 279000, A
91	40	75.5	310	3	US-09-815-242-10667	Sequence 10667, A
92	40	75.5	410	5	US-10-732-923-10238	Sequence 10238, A
93	40	75.5	669	6	US-11-097-143-36501	Sequence 36501, A
94	39	73.6	166	4	US-10-437-963-190870	Sequence 190870, A
95	39	73.6	692	3	US-09-826-115-22	Sequence 22, Appl
96	39	73.6	692	5	US-10-500-796A-22	Sequence 22, Appl
97	39	73.6	853	4	US-10-437-963-122232	Sequence 122232, A
98	38	71.7	41	3	US-09-881-710-27	Sequence 27, Appl
99	38	71.7	41	4	US-10-634-895-27	Sequence 27, Appl
100	38	71.7	71	4	US-10-311-213-13	Sequence 13, Appl
101	38	71.7	132	5	US-10-425-115-328599	Sequence 328599, A
102	38	71.7	147	4	US-10-424-599-241346	Sequence 241346, A
103	38	71.7	217	4	US-10-127-032-113	Sequence 113, App
104	38	71.7	218	4	US-10-425-115-311873	Sequence 311873, A
105	38	71.7	248	4	US-10-032-585-7603	Sequence 7603, Ap
106	38	71.7	257	3	US-09-944-849-5	Sequence 5, Appl
107	38	71.7	261	6	US-10-756-149-5274	Sequence 5274, Ap
108	38	71.7	261	6	US-11-097-143-30573	Sequence 30573, A
109	38	71.7	281	4	US-10-282-122A-67206	Sequence 67206, A
110	38	71.7	379	3	US-09-996-606-2	Sequence 2, Appl
111	38	71.7	379	4	US-10-642-297-2	Sequence 2, Appl
112	38	71.7	429	4	US-10-156-761-11695	Sequence 11695, A
113	38	71.7	649	6	US-11-097-143-36498	Sequence 36498, A
114	38	71.7	684	5	US-10-679-520A-55	Sequence 55, Appl
115	38	71.7	684	5	US-10-679-520A-57	Sequence 57, Appl
116	38	71.7	684	5	US-10-679-520A-61	Sequence 61, Appl
117	38	71.7	686	5	US-10-679-520A-59	Sequence 59, Appl
118	38	71.7	692	3	US-09-826-115-16	Sequence 16, Appl
119	38	71.7	692	5	US-10-500-796A-16	Sequence 16, Appl
120	38	71.7	945	4	US-10-437-963-171001	Sequence 171001, A
121	38	71.7	2075	6	US-11-097-143-11823	Sequence 11823, A
122	38	71.7	3430	4	US-10-224-999A-3473	Sequence 3473, Ap
123	38	71.7	3433	4	US-10-679-520A-67	Sequence 67, Appl
124	38	71.7	3433	5	US-10-956-085-2	Sequence 2, Appl
125	38	71.7	3433	5	US-10-956-085-2	Sequence 2, Appl
126	38	71.7	3433	5	US-10-956-085-12	Sequence 12, Appl
127	38	71.7	4746	4	US-10-369-493-433	Sequence 433, App
128	37	69.8	51	4	US-10-437-963-102911	Sequence 102911, A
129	37	69.8	59	4	US-10-424-599-156609	Sequence 156609, A
130	37	69.8	83	4	US-10-424-599-230978	Sequence 230978, A
131	37	69.8	85	4	US-10-424-599-266809	Sequence 266809, A
132	37	69.8	124	4	US-10-424-599-226470	Sequence 226470, A
133	37	69.8	227	4	US-10-259-165-100	Sequence 100, App
134	37	69.8	227	4	US-10-259-165-432	Sequence 432, App
135	37	69.8	246	4	US-10-425-115-207892	Sequence 207892, A
136	37	69.8	257	4	US-10-437-963-127257	Sequence 127257, A
137	37	69.8	258	4	US-10-437-963-114079	Sequence 114079, A
138	37	69.8	266	4	US-10-437-963-109217	Sequence 109217, A
139	37	69.8	306	4	US-10-369-493-11927	Sequence 11927, A
140	37	69.8	341	4	US-10-408-765A-1952	Sequence 1952, Ap
141	37	69.8	350	4	US-10-424-599-182862	Sequence 182862, A
142	37	69.8	375	4	US-10-424-599-169020	Sequence 169020, A
143	37	69.8	386	4	US-10-276-774-2362	Sequence 2362, Ap
144	37	69.8	438	4	US-10-425-115-334872	Sequence 334872, A
145	37	69.8	440	5	US-10-732-923-8259	Sequence 8259, Ap
146	37	69.8	442	5	US-10-732-923-8250	Sequence 8250, Ap
147	37	69.8	453	4	US-10-437-963-109214	Sequence 109214, A
148	37	69.8	506	4	US-10-108-260A-4592	Sequence 4592, Ap
149	37	69.8	518	4	US-10-230-026-24	Sequence 24, Appl
150	37	69.8	518	5	US-10-486-307-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
 US-10-608-147-29
 ; Sequence 29, Application US/10608147
 ; Publication No. US20050080231A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DESPRES, Philippe
 ; TITLE OF INVENTION: SMALL PEPTIDES HAVING APOPTOTIC ACTIVITIES AND THEIR APPLICATIONS
 ; FILE REFERENCE: 239786USOCIP
 ; CURRENT APPLICATION NUMBER: US/10/608, 147
 ; CURRENT FILING DATE: 2003-06-30
 ; PRIOR APPLICATION NUMBER: US 10/311, 213
 ; PRIOR FILING DATE: 2003-05-19
 ; PRIOR APPLICATION NUMBER: PCT/IB01/01570
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: US 60/212,129
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 29
 ; LENGTH: 9
 ; TYPE: PPT
 ; ORGANISM: Dengue virus type 2
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Peptide of the M protein conferring apoptotic activity

US-10-608-147-29

Query Match 100.0%; Score 53; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
| | | | | | | | |
Db 1 IETWILRHP 9

RESULT 2

US-10-608-147-36

; Sequence 36, Application US/10608147

; Publication No. US20050080231A1

; GENERAL INFORMATION:

; APPLICANT: DESPRES, Philippe

; APPLICANT: CATTEAU, Adeline

; TITLE OF INVENTION: SMALL PEPTIDES HAVING APOPTOTIC ACTIVITIES AND THEIR APPLICATIONS

; FILE REFERENCE: 239786USOCIP

; CURRENT APPLICATION NUMBER: US/10/608,147

; CURRENT FILING DATE: 2003-06-30

; PRIOR APPLICATION NUMBER: US 10/311,213

; PRIOR FILING DATE: 2003-05-19

; PRIOR APPLICATION NUMBER: PCT/IB01/01570

; PRIOR FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: US 60/212,129

; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 36

; LENGTH: 21

; TYPE: PRT

; ORGANISM: Dengue virus type 2

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: M20-40/DEN-2

US-10-608-147-36

Query Match 100.0%; Score 53; DB 5; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
| | | | | | | | |
Db 13 IETWILRHP 21

RESULT 3

US-10-608-147-35

; Sequence 35, Application US/10608147

; Publication No. US20050080231A1

; GENERAL INFORMATION:

; APPLICANT: DESPRES, Philippe

; APPLICANT: CATTEAU, Adeline

; TITLE OF INVENTION: SMALL PEPTIDES HAVING APOPTOTIC ACTIVITIES AND THEIR APPLICATIONS

; FILE REFERENCE: 239786USOCIP

; CURRENT APPLICATION NUMBER: US/10/608,147

; CURRENT FILING DATE: 2003-06-30

; PRIOR APPLICATION NUMBER: US 10/311,213

; PRIOR FILING DATE: 2003-05-19

; PRIOR APPLICATION NUMBER: PCT/IB01/01570

; PRIOR FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: US 60/212,129

; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 36

; LENGTH: 21

; TYPE: PRT

; ORGANISM: Dengue virus type 2

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: M20-40/DEN-2

US-10-608-147-36

Query Match 100.0%; Score 53; DB 5; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; TITLE OF INVENTION: SMALL PEPTIDES HAVING APOPTOTIC ACTIVITIES AND THEIR APPLICATIONS

; FILE REFERENCE: 239786USOCIP

; CURRENT APPLICATION NUMBER: US/10/608,147

; CURRENT FILING DATE: 2003-06-30

; PRIOR APPLICATION NUMBER: US 10/311,213

; PRIOR FILING DATE: 2003-05-19

; PRIOR APPLICATION NUMBER: PCT/IB01/01570

; PRIOR FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: US 60/212,129

; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 35

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Dengue virus type 2

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: M9-40/DEN-2

US-10-608-147-35

Query Match 100.0%; Score 53; DB 5; Length 32;

Best Local Similarity 100.0%; Pred. No. 0.17;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
| | | | | | | | |
Db 24 IETWILRHP 32

RESULT 4

US-10-608-029-23

; Sequence 23, Application US/10608029

; Publication No. US20040266987A1

; GENERAL INFORMATION:

; APPLICANT: DESPRES, PHILLIPE

; APPLICANT: CATTEAU, ADELIN

; TITLE OF INVENTION: ATTENUATED FLAVIVIRUS STRAINS CONTAINING A MUTATED M-ECTODOMAN

; FILE REFERENCE: 239783USO

; CURRENT APPLICATION NUMBER: US/10/608,029

; CURRENT FILING DATE: 2003-06-30

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 23

; LENGTH: 39

; TYPE: PRT

; ORGANISM: Dengue virus

US-10-608-029-23

Query Match 100.0%; Score 53; DB 5; Length 39;

Best Local Similarity 100.0%; Pred. No. 0.2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
| | | | | | | | |
Db 24 IETWILRHP 32

Db 31 IETWILRHP 39

RESULT 5
US-10-311-213-3
; Sequence 3, Application US/10311213
; Publication No. US20040101862A1
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Philippe
; APPLICANT: COURAGEOT, Marie-Pierre
; APPLICANT: DEUBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEINS.
; FILE REFERENCE: 231164US0PCT
; CURRENT APPLICATION NUMBER: US/10/311,213
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/IB01/01570
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Dengue virus type 2
US-10-311-213-3

Query Match 100.0%; Score 53; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IETWILRHP 9
Db 32 IETWILRHP 40

RESULT 6
US-10-608-029-25
; Sequence 25, Application US/10608029
; Publication No. US20040266987A1
; GENERAL INFORMATION:
; APPLICANT: DESPRES, PHILIPPE
; APPLICANT: CATTEAU, ADELIN
; TITLE OF INVENTION: ATTENUATED FLAVIVIRUS STRAINS CONTAINING A MUTATED M-ECTODOMAN
; TITLE OF INVENTION: AND THEIR APPLICATIONS
; FILE REFERENCE: 239783US0
; CURRENT APPLICATION NUMBER: US/10/608,029
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 40
; TYPE: PRT

; ORGANISM: Dengue virus
US-10-608-029-25

Query Match 100.0%; Score 53; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IETWILRHP 9
Db 32 IETWILRHP 40

RESULT 7
US-10-608-147-31
; Sequence 31, Application US/10608147
; Publication No. US20050080231A1
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Philippe
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: SMALL PEPTIDES HAVING APOPTOTIC ACTIVITIES AND THEIR APPLICATIONS
; FILE REFERENCE: 239786US0CIP
; CURRENT APPLICATION NUMBER: US/10/608,147
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: US 10/311,213
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: PCT/IB01/01570
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Dengue virus type 2
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: M1-40/DEN-2
US-10-608-147-31

Query Match 100.0%; Score 53; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IETWILRHP 9
Db 32 IETWILRHP 40

RESULT 8
US-10-311-213-32
; Sequence 32, Application US/10311213
; Publication No. US20040101862A1
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Philippe
; APPLICANT: COURAGEOT, Marie-Pierre

```
; APPLICANT: DEUBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE
GLYCOPROTEINS.
; FILE REFERENCE: 23164US0PCT
; CURRENT APPLICATION NUMBER: US/10/311,213
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/IB01/01570
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Dengue virus type 2
US-10-311-213-32
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Query Match          100.0%; Score 53; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 IETWILRHP 9
    |||||||
DB 40 IETWILRHP 48
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RESULT 9
US-10-375-932-122
; Sequence 122, Application US/10375932
; Publication No. US2004009469A1
; GENERAL INFORMATION:
; APPLICANT: Apt, Doris
; APPLICANT: Punnonen, Juha
; APPLICANT: Brinkman, Alice M.
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
; FILE REFERENCE: 0322.210US
; CURRENT APPLICATION NUMBER: US/10/375,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,030
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 345
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide: 23C12 REST OF C15/PRM
US-10-375-932-122
```

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Query Match          100.0%; Score 53; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 IETWILRHP 9
```

```
DB 139 IETWILRHP 147
```

```
RESULT 10
US-10-375-932-118
; Sequence 118, Application US/10375932
; Publication No. US2004009469A1
; GENERAL INFORMATION:
; APPLICANT: Apt, Doris
; APPLICANT: Punnonen, Juha
; APPLICANT: Brinkman, Alice M.
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
; FILE REFERENCE: 0322.210US
; CURRENT APPLICATION NUMBER: US/10/375,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,030
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 345
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Dengue virus type 2
; FEATURE:
; OTHER INFORMATION: DEN-2 REST OF C15/PRM
US-10-375-932-118
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```
Query Match          100.0%; Score 53; DB 4; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 IETWILRHP 9
    |||||||
DB 143 IETWILRHP 151
```

```
RESULT 11
US-10-375-932-121
; Sequence 121, Application US/10375932
; Publication No. US2004009469A1
; GENERAL INFORMATION:
; APPLICANT: Apt, Doris
; APPLICANT: Punnonen, Juha
; APPLICANT: Brinkman, Alice M.
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
; FILE REFERENCE: 0322.210US
; CURRENT APPLICATION NUMBER: US/10/375,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,030
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 345
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide: 21C1 REST OF C15/PRM
US-10-375-932-121

Query Match          100.0%; Score 53; DB 4; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IETWILRHP 9
        |||||||||
Db       143 IETWILRHP 151

RESULT 12
US-10-375-932-143
; Sequence 143, Application US/10375932
; Publication No. US20040009469A1
; GENERAL INFORMATION:
; APPLICANT: Apt, Doris
; APPLICANT: Punnonen, Juha
; APPLICANT: Brinkman, Alice M.
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
; FILE REFERENCE: 0322.210US
; CURRENT APPLICATION NUMBER: US/10/375,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,030
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 345
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide: 23C12(C15/full prM/full E)
US-10-375-932-143

Query Match          100.0%; Score 53; DB 4; Length 675;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IETWILRHP 9
        |||||||||
Db       139 IETWILRHP 147

RESULT 13
US-10-375-932-237
; Sequence 237, Application US/10375932
; Publication No. US20040009469A1
; GENERAL INFORMATION:
; APPLICANT: Apt, Doris
; APPLICANT: Punnonen, Juha
; APPLICANT: Brinkman, Alice M.
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
; FILE REFERENCE: 0322.210US
; CURRENT APPLICATION NUMBER: US/10/375,932

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; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,030
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 345
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide: 25B10 (C15/full length prM/full length E)
US-10-375-932-237

Query Match          100.0%; Score 53; DB 4; Length 675;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IETWILRHP 9
        |||||||||
Db       139 IETWILRHP 147

RESULT 14
US/10/375
; Sequence 251, Application US/10375932
; Publication No. US20040009469A1
; GENERAL INFORMATION:
; APPLICANT: Apt, Doris
; APPLICANT: Punnonen, Juha
; APPLICANT: Brinkman, Alice M.
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
; FILE REFERENCE: 0322.210US
; CURRENT APPLICATION NUMBER: US/10/375,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,030
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 345
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 251
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide: 16G11-25B10ext (16G11 extended to C15/full length prM/full length E with 25B10 residues-of-E-protein-US/10/375,932-251)

Query Match          100.0%; Score 53; DB 4; Length 675;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IETWILRHP 9
        |||||||||
Db       139 IETWILRHP 147

```

```

RESULT 15
US-10/375
; Sequence 253, Application US/10375932
; Publication No. US20040009469A1
; GENERAL INFORMATION:
; APPLICANT: Apt, Doris
; APPLICANT: Brinkman, Juha
; APPLICANT: Brinkman, Alice M.
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
; FILE REFERENCE: 0322.210US
; CURRENT APPLICATION NUMBER: US/10/375,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,030
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 345
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide: 18H6-25B10ext (18H6 extended to
C15/full length prM/full length E with 25B10 residues-of-E-protein-
US/10/375,932-253

Query Match          100.0%; Score 53; DB 4; Length 675;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  IETWILRHP 9
        |||||||||
Db       139 IETWILRHP 147

RESULT 16
US-10-375-932-238
; Sequence 238, Application US/10375932
; Publication No. US20040009469A1
; GENERAL INFORMATION:
; APPLICANT: Apt, Doris
; APPLICANT: Brinkman, Juha
; APPLICANT: Brinkman, Alice M.
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
; FILE REFERENCE: 0322.210US
; CURRENT APPLICATION NUMBER: US/10/375,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,030
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 345
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide: 25D4 (C15/full length prM/full
length E)

```

```

US-10-375-932-238

Query Match          100.0%; Score 53; DB 4; Length 677;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  IETWILRHP 9
        |||||||||
Db       139 IETWILRHP 147

RESULT 17
US-10-375-932-142
; Sequence 142, Application US/10375932
; Publication No. US20040009469A1
; GENERAL INFORMATION:
; APPLICANT: Apt, Doris
; APPLICANT: Brinkman, Juha
; APPLICANT: Brinkman, Alice M.
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
; FILE REFERENCE: 0322.210US
; CURRENT APPLICATION NUMBER: US/10/375,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,030
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 345
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide: 21C1 (C15/full prM/full E)
US-10-375-932-142

Query Match          100.0%; Score 53; DB 4; Length 681;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  IETWILRHP 9
        |||||||||
Db       143 IETWILRHP 151

RESULT 18
US-10-375-932-228
; Sequence 228, Application US/10375932
; Publication No. US20040009469A1
; GENERAL INFORMATION:
; APPLICANT: Apt, Doris
; APPLICANT: Brinkman, Juha
; APPLICANT: Brinkman, Alice M.
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
; FILE REFERENCE: 0322.210US
; CURRENT APPLICATION NUMBER: US/10/375,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,030

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; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 345
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 228
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Dengue virus type 2
; FEATURE:
; OTHER INFORMATION: DEN-2 \C15/full prn/full E parent
US-10-375-932-228

Query Match          100.0%; Score 53; DB 4; Length 681;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 1ETWLRHP 9
        |||||||||
Db       143 1ETWLRHP 151

RESULT 19
US-10-500-796A-43
; Sequence 43, Application US/10500796A
; Publication No. US20050163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services, Centers for Disease Control and Prevention
; APPLICANT: Chang, Gwong-Jen J.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS
INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500,796A
; CURRENT FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 43
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-500-796A-43

Query Match          100.0%; Score 53; DB 5; Length 685;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 1ETWLRHP 9
        |||||||||
Db       147 1ETWLRHP 155

RESULT 20
US-10-500-796A-45
; Sequence 45, Application US/10500796A
; Publication No. US20050163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services, Centers for Disease Control and Prevention
; APPLICANT: Chang, Gwong-Jen J.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS
INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500,796A
; CURRENT FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-500-796A-45

Query Match          100.0%; Score 53; DB 5; Length 685;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 1ETWLRHP 9
        |||||||||
Db       147 1ETWLRHP 155

RESULT 21
US-10-500-796A-47
; Sequence 47, Application US/10500796A
; Publication No. US20050163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services, Centers for Disease Control and Prevention
```

```

; APPLICANT: Chang, Gwang-Jen J.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS
; INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500,796A
; CURRENT FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 47
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-500-796A-47

Query Match          100.0%; Score 53; DB 5; Length 685;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 1ETWILRHP 9
        1111111111
Db      147 1ETWILRHP 155

RESULT 22
US-10-247-960-3
; Sequence 3, Application US/10247960
; Publication No. US20030175304A1
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beeth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
; FILE REFERENCE: 24733-20005.01
; CURRENT APPLICATION NUMBER: US/10/247,960
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/376,463
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0

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```

; SEQ ID NO 3
; LENGTH: 1127
; TYPE: PRT
; ORGANISM: Dengue virus
US-10-247-960-3

Query Match          100.0%; Score 53; DB 4; Length 1127;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 1ETWILRHP 9
        1111111111
Db      237 1ETWILRHP 245

RESULT 23
US-10-719-547-17
; Sequence 17, Application US/10719547
; Publication No. US20050010043A1
; GENERAL INFORMATION:
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; TITLE OF INVENTION: ATTENUATING DENGUE VIRUSES AND CHIMERIC DENGUE VIRUSES
; FILE REFERENCE: NIH214.001C1
; CURRENT APPLICATION NUMBER: US/10/719,547
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/16308
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293049
; PRIOR FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 3388
; TYPE: PRT
; ORGANISM: Recombinant Dengue rDEN2/4d30
US-10-719-547-17

Query Match          100.0%; Score 53; DB 5; Length 3388;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 1ETWILRHP 9
        1111111111
Db      237 1ETWILRHP 245

RESULT 24
US-10-719-547-21
; Sequence 21, Application US/10719547
; Publication No. US20050010043A1
; GENERAL INFORMATION:
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Murphy, Brian R.

```



```
; APPLICANT: Hanley, Kathryn A.
; APPLICANT: Blaney, Joseph E. Jr.
; TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
; FILE REFERENCE: NIH214.001C1
; CURRENT APPLICATION NUMBER: US/10/719,547
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/16308
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293049
; PRIOR FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 3391
; TYPE: PRT
; ORGANISM: Dengue 2 virus strain NGC
US-10-719-547-21
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```
Query Match      100.0%; Score 53; DB 5; Length 3391;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IETWILRHP 9
        |||||||||
Db      237 IETWILRHP 245
```

```
RESULT 25
US-10-871-775-31
; Sequence 31, Application US/10871775
; Publication No. US2005010086A1
; GENERAL INFORMATION:
; APPLICANT: Pletnov, Alexander
; APPLICANT: Putnak, Joseph Robert
; APPLICANT: Chanock, Robert M.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Whitehead, Stephen S.
; APPLICANT: Blaney, Joseph E., Jr.
; TITLE OF INVENTION: CONSTRUCTION OF WEST NILE VIRUS AND
; TITLE OF INVENTION: DENGUE VIRUS CHIMERAS FOR USE IN A LIVE VIRUS VACCINE TO
; FILE REFERENCE: NIH225.001C1
; CURRENT APPLICATION NUMBER: US/10/871,775
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: PCT/US03/00594
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/347,281
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 3391
; TYPE: PRT
; ORGANISM: Dengue 2 (Tonga/74)
US-10-871-775-31
```

```
Query Match      100.0%; Score 53; DB 5; Length 3391;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IETWILRHP 9
        |||||||||
Db      237 IETWILRHP 245
```

Search completed: January 30, 2006, 09:18:53
Job time : 62 secs

OM protein - protein search, using sw model

Run on: January 30, 2006, 09:09:58 ; Search time 48 Seconds

(without alignments)
16.535 Million cell updates/sec

Title: US-10-608-147-29

Perfect score: 53

Sequence: 1 LETWILRHP 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/laa/5 COMB.pep:*
- 2: /cgn2_6/ptodata/1/laa/6 COMB.pep:*
- 3: /cgn2_6/ptodata/1/laa/H COMB.pep:*
- 4: /cgn2_6/ptodata/1/laa/PCTUS COMB.pep:*
- 5: /cgn2_6/ptodata/1/laa/RE COMB.pep:*
- 6: /cgn2_6/ptodata/1/laa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	635	2	US-09-341-833A-7
2	53	100.0	677	2	US-09-341-833A-8
3	53	100.0	1127	2	US-08-937-195-3
4	53	100.0	1127	2	US-08-915-152-3
5	53	100.0	1127	2	US-09-376-463-3
6	53	100.0	1127	4	PCT-US96-07627-3
7	48	90.6	40	2	US-09-881-710-29
8	47	88.7	40	2	US-09-881-710-28
9	47	88.7	76	2	US-09-891-710-1
10	47	88.7	661	2	US-09-452-638-51
11	47	88.7	661	2	US-09-121-587A-2

12	41	77.4	635	2	US-09-341-833A-9	Sequence 9, Appli
13	40	75.5	39	2	US-09-881-710-12	Sequence 12, Appli
14	40	75.5	39	2	US-09-881-710-30	Sequence 30, Appli
15	40	75.5	316	2	US-09-134-000C-5598	Sequence 5598, Ap
16	39	73.6	85	2	US-09-107-532A-4082	Sequence 4082, Ap
17	38	71.7	41	2	US-09-881-710-27	Sequence 27, Appli
18	38	71.7	219	2	US-09-248-796A-15621	Sequence 15621, A
19	38	71.7	230	2	US-09-252-991A-22207	Sequence 22207, A
20	38	71.7	248	2	US-09-258-634-4	Sequence 4, Appli
21	38	71.7	416	2	US-09-252-991A-32875	Sequence 32875, A
22	37	69.8	260	2	US-09-252-991A-23866	Sequence 23866, A
23	37	69.8	548	2	US-10-104-047-3500	Sequence 3500, Ap
24	37	69.8	1351	2	US-09-489-039A-11032	Sequence 11032, A
25	36	67.9	315	2	US-09-270-767-56647	Sequence 56647, A
26	36	67.9	324	2	US-09-489-039A-7896	Sequence 7896, Ap
27	36	67.9	343	2	US-09-252-991A-31075	Sequence 31075, A
28	36	67.9	346	2	US-09-248-796A-18974	Sequence 18974, A
29	36	67.9	411	2	US-09-270-767-41426	Sequence 41426, A
30	35	66.0	76	2	US-08-554-840-21	Sequence 21, Appli
31	35	66.0	76	2	US-08-925-338-21	Sequence 21, Appli
32	35	66.0	76	2	US-09-332-595-21	Sequence 21, Appli
33	35	66.0	125	2	US-09-328-352-5320	Sequence 5320, Ap
34	35	66.0	135	2	US-09-270-767-61883	Sequence 61883, A
35	35	66.0	139	2	US-09-198-452A-735	Sequence 735, App
36	35	66.0	162	2	US-09-252-991A-26062	Sequence 26062, A
37	35	66.0	305	2	US-09-252-991A-22922	Sequence 22922, A
38	35	66.0	311	2	US-09-489-039A-9550	Sequence 9550, Ap
39	35	66.0	334	2	US-09-270-767-38437	Sequence 38437, A
40	35	66.0	334	2	US-09-270-767-53654	Sequence 53654, A
41	35	66.0	366	2	US-09-489-039A-12929	Sequence 12929, A
42	35	66.0	373	2	US-09-270-767-46313	Sequence 46313, A
43	35	66.0	388	2	US-10-126-279-6	Sequence 6, Appli
44	35	66.0	388	2	US-10-286-606-6	Sequence 6, Appli
45	35	66.0	432	2	US-09-328-352-6119	Sequence 6119, Ap
46	35	66.0	443	2	US-09-543-681A-5826	Sequence 5826, Ap
47	35	66.0	444	2	US-09-328-352-6463	Sequence 6463, Ap
48	35	66.0	447	2	US-09-252-991A-32907	Sequence 32907, A
49	35	66.0	455	2	US-09-252-991A-18265	Sequence 18265, A
50	35	66.0	824	2	US-09-711-164-377	Sequence 377, App
51	35	66.0	970	6	5229293-2	Sequence 13, Appli
52	35	66.0	3421	2	US-09-452-638-53	Sequence 53, Appli
53	35	66.0	3421	2	US-09-121-587A-13	Sequence 13, Appli
54	35	66.0	3443	1	US-08-416-603-2	Sequence 2, Appli
55	34	64.2	70	2	US-09-248-796A-26491	Sequence 26491, A
56	34	64.2	96	2	US-08-851-362D-27	Sequence 27, Appli
57	34	64.2	100	2	US-09-270-767-60810	Sequence 60810, A
58	34	64.2	117	2	US-08-851-362D-44	Sequence 44, Appli
59	34	64.2	117	2	US-10-330-613A-13	Sequence 13, Appli
60	34	64.2	134	2	US-09-107-433-4903	Sequence 4903, Ap
61	34	64.2	137	2	US-09-270-767-45315	Sequence 45315, A
62	34	64.2	164	2	US-09-328-352-5068	Sequence 5068, Ap
63	34	64.2	237	2	US-09-252-991A-21759	Sequence 21759, A
64	34	64.2	239	2	US-09-489-039A-13019	Sequence 13019, A
65	34	64.2	256	2	US-08-478-316-11	Sequence 11, Appli
66	34	64.2	256	2	US-09-113-750A-37	Sequence 37, Appli
67	34	64.2	256	2	US-09-019-793A-11	Sequence 11, Appli
68	34	64.2	256	2	US-09-601-326-11	Sequence 11, Appli

69	34	64.2	262	2	US-09-252-991A-30480	Sequence 30480, A
70	34	64.2	273	2	US-09-252-991A-28278	Sequence 28278, A
71	34	64.2	288	2	US-08-995-280C-2	Sequence 2, Appli
72	34	64.2	288	2	US-09-215-042-2	Sequence 2, Appli
73	34	64.2	308	2	US-09-583-110-2746	Sequence 2746, Ap
74	34	64.2	347	2	US-09-489-039A-11579	Sequence 11579, A
75	34	64.2	385	2	US-09-543-681A-4674	Sequence 4674, Ap
76	34	64.2	390	2	US-08-555-755C-4	Sequence 4, Appli
77	34	64.2	415	2	US-09-896-866B-7	Sequence 7, Appli
78	34	64.2	433	2	US-09-896-866B-1	Sequence 1, Appli
79	34	64.2	476	2	US-08-378-313-34	Sequence 34, Appli
80	34	64.2	485	2	US-08-378-313-25	Sequence 25, Appli
81	34	64.2	485	2	US-08-378-313-27	Sequence 27, Appli
82	34	64.2	485	2	US-08-378-313-32	Sequence 32, Appli
83	34	64.2	488	1	US-08-695-412B-10	Sequence 10, Appli
84	34	64.2	488	2	US-09-253-154D-10	Sequence 10, Appli
85	34	64.2	488	2	US-10-213-452A-10	Sequence 6, Appli
86	34	64.2	490	1	US-08-724-194-6	Sequence 8064, Ap
87	34	64.2	1065	2	US-09-328-352-8064	Sequence 24533, A
88	34	64.2	1069	2	US-09-252-991A-24533	Sequence 20395, A
89	34	64.2	1627	2	US-09-252-991A-20395	Sequence 21617, A
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91	33	62.3	14	2	US-09-513-999C-6236	Sequence 6236, Ap
92	33	62.3	56	2	US-09-621-976-4309	Sequence 4309, Ap
93	33	62.3	68	2	US-09-513-999C-7489	Sequence 7489, Ap
94	33	62.3	117	2	US-09-270-767-43675	Sequence 43675, A
95	33	62.3	120	2	US-09-270-767-38604	Sequence 38604, A
96	33	62.3	124	2	US-09-270-767-53821	Sequence 53821, A
97	33	62.3	124	2	US-09-252-991A-16591	Sequence 16591, A
98	33	62.3	209	2	US-09-107-532A-3856	Sequence 33067, A
99	33	62.3	247	2	US-09-270-767-33067	Sequence 48284, A
100	33	62.3	258	2	US-09-270-767-48284	Sequence 26022, A
101	33	62.3	238	2	US-09-252-991A-26022	Sequence 32703, A
102	33	62.3	271	2	US-09-270-767-32703	Sequence 623, App
103	33	62.3	285	2	US-09-614-221A-623	Sequence 20663, A
104	33	62.3	300	2	US-09-248-796A-20663	Sequence 21273, A
105	33	62.3	328	2	US-09-248-796A-21273	Sequence 45255, A
106	33	62.3	340	2	US-09-328-352-7736	Sequence 7736, Ap
107	33	62.3	377	2	US-08-549-004A-5	Sequence 5, Appli
108	33	62.3	382	1	US-09-051-982A-5	Sequence 45717, A
109	33	62.3	401	1	US-09-949-016-9950	Sequence 7950, Ap
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112	33	62.3	424	2	US-09-252-991A-2	Sequence 2, Appli
113	33	62.3	455	2	US-09-446-504-64	Sequence 64, Appli
114	33	62.3	467	1	US-09-712-266-64	Sequence 45060, A
115	33	62.3	467	1	US-09-252-991A-21553	Sequence 21553, A
116	33	62.3	469	2	US-09-949-016-11571	Sequence 11571, A
117	33	62.3	479	2	US-10-104-047-2552	Sequence 2552, Ap
118	33	62.3	479	2	US-08-592-646A-54	Sequence 54, Appli
119	33	62.3	502	2	US-09-165-422-54	Sequence 54, Appli
120	33	62.3	681	2	US-09-270-767-45060	Sequence 59608, A
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124	32	60.4	15	2	US-09-165-422-54	
125	32	60.4	43	2	US-09-270-767-59608	

126	32	60.4	51	2	US-09-513-999C-7146	Sequence 7146, Ap
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128	32	60.4	99	2	US-09-492-709A-335	Sequence 335, App
129	32	60.4	138	2	US-08-763-620-13	Sequence 13, Appli
130	32	60.4	139	2	US-08-897-076-13	Sequence 13, Appli
131	32	60.4	139	2	US-09-543-681A-6577	Sequence 6577, Ap
132	32	60.4	139	2	US-09-205-658-13	Sequence 13, Appli
133	32	60.4	178	2	US-09-267-963D-33	Sequence 33, Appli
134	32	60.4	183	2	US-09-489-039A-10898	Sequence 10898, A
135	32	60.4	281	2	US-09-252-991A-30415	Sequence 30415, A
136	32	60.4	286	2	US-08-818-112-81	Sequence 81, Appli
137	32	60.4	286	2	US-08-818-112-82	Sequence 82, Appli
138	32	60.4	286	2	US-09-056-556-81	Sequence 81, Appli
139	32	60.4	286	2	US-09-072-596-82	Sequence 82, Appli
140	32	60.4	286	2	US-09-072-596-81	Sequence 81, Appli
141	32	60.4	311	2	US-10-193-002-82	Sequence 82, Appli
142	32	60.4	286	2	US-10-084-843-81	Sequence 81, Appli
143	32	60.4	291	2	US-09-489-039A-8172	Sequence 8172, Ap
144	32	60.4	296	2	US-09-107-532A-4943	Sequence 4943, Ap
145	32	60.4	306	2	US-09-487-558B-84	Sequence 84, Appli
146	32	60.4	311	2	US-09-710-279-1260	Sequence 1260, Ap
147	32	60.4	327	2	US-10-360-101-255	Sequence 255, App
148	32	60.4	343	2	US-09-134-001C-5484	Sequence 5484, Ap
149	32	60.4	345	2	US-09-120-366-73	Sequence 73, Appli
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ALIGNMENTS

RESULT 1
 US-09-341-833A-7
 ; Sequence 7, Application US/09341833A
 ; Patent No. 6383488
 ; GENERAL INFORMATION:
 ; APPLICANT: CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA
 ; TITLE OF INVENTION: PRE-M/M PROTEIN EPTIOPES OF THE DENGUE VIRUS, SYNTHETIC
 ; FILE REFERENCE: Dengue preW/M SEQs 1-9 for 976-4(0003)
 ; CURRENT FILING DATE: 1999-10-14
 ; PRIOR APPLICATION NUMBER: US/09/341, 833A
 ; PRIOR FILING DATE: 1997-01-15
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 635
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
 ; OTHER INFORMATION: of Dengue virus preW/M and Neisseria meningitidis
 ; OTHER INFORMATION: P64k protein.
 US-09-341-833A-7
 Query Match 100.0%; Score 53; DB 2; Length 635;
 Best Local Similarity 100.0%; Pred. No. 0.35;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IETWILRHP 9
Db 74 IETWILRHP 82

RESULT 2
US-09-341-833A-8
; Sequence 8, Application US/09341833A
; Patent No. 6383488
; GENERAL INFORMATION:
; APPLICANT: CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA
; TITLE OF INVENTION: PRE-M/M PROTEIN EPITOPES OF THE DENGUE VIRUS, SYNTHETIC
; TITLE OF INVENTION: PEPTIDES AND THEIR USES
; FILE REFERENCE: Dengue prem/M SEQs 1-9 for 976-4(0003)
; CURRENT FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: US/09/341,833A
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
; OTHER INFORMATION: of Dengue virus prem/M and Neisseria meningitidis
US-09-341-833A-8

Query Match 100.0%; Score 53; DB 2; Length 677;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IETWILRHP 9
Db 116 IETWILRHP 124

RESULT 3
US-08-937-195-3
; Sequence 3, Application US/08937195
; Patent No. 6136561
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA

; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,195
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/488,807
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-937-195-3

Query Match 100.0%; Score 53; DB 2; Length 1127;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IETWILRHP 9
Db 237 IETWILRHP 245

RESULT 4
US-08-915-152-3
; Sequence 3, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; APPLICANT: CLEMENTS, DAVID
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-915-152-3

Query Match          100.0%; Score 53; DB 2; Length 1127;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 1ETWILRHP 9
Db 237 1ETWILRHP 245

RESULT 5
US-09-376-463-3
; Sequence 3, Application US/09376463
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
; FILE REFERENCE: 24733-20005.20
; CURRENT APPLICATION NUMBER: US/09/376,463
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1127

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; TYPE: PRT
; ORGANISM: Dengue virus
; US-09-376-463-3

Query Match          100.0%; Score 53; DB 2; Length 1127;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 1ETWILRHP 9
Db 237 1ETWILRHP 245

RESULT 6
PCT-US96-07627-3
; Sequence 3, Application PC/TUS9607627
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
; NUMBER OF SEQUENCES: 50
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/07627
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-07627-3

Query Match          100.0%; Score 53; DB 4; Length 1127;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 1ETWILRHP 9
Db 237 1ETWILRHP 245

Search completed: January 30, 2006, 09:17:41
Job time : 47 secs

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OM protein - protein search, using sw model

Run on: January 30, 2006, 08:59:57 ; Search time 134 Seconds

(Without alignments)
29.511 Million cell updates/sec

Title: US-10-608-147-29

Perfect score: 53

Sequence: 1 IETWILRHP 9

Scoring table: BLOSUM62

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Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

1: Geneseq_21:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	53	100.0	32	ADM12593	Adm12593 M1-40/DE
4	53	100.0	39	ADM12576	Adm12576 M1-40/DEN
5	53	100.0	40	AAE17432	AAe17432 Dengue (D
6	53	100.0	40	ADM12578	Adm12578 M1-40/YF.
7	53	100.0	48	AAE17433	AAe17433 (95-114)E
8	53	100.0	167	ADM37497	Adh37497 Dengue vi
9	53	100.0	171	ADM37493	Adh37493 Dengue vi
10	53	100.0	171	ADM37496	Adh37496 Dengue vi
11	53	100.0	635	AAW75410	AAw75410 Fusion pr
12	53	100.0	675	ADM37628	Adh37628 Dengue vi
13	53	100.0	675	ADM37518	Adh37518 Dengue vi
14	53	100.0	675	ADM37612	Adh37612 Dengue vi
15	53	100.0	675	ADM37626	Adh37626 Dengue vi
16	53	100.0	677	AAW75411	AAw75411 Fusion pr
17	53	100.0	677	ADM37613	Adh37613 Dengue vi
18	53	100.0	681	ADM37603	Adh37603 Dengue vi
19	53	100.0	681	ADM37517	Adh37517 Dengue vi
20	53	100.0	685	ABP57874	ABp57874 Plasmid P
21	53	100.0	685	ABP57876	ABp57876 Plasmid P
22	53	100.0	685	ABP57875	ABp57875 Plasmid P
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24	53	100.0	1127	AAW05522	AAy05522 Dengue vi
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28	53	100.0	3391	AAH13166	AAh13166 Proteins
29	53	100.0	3391	AAW06591	AAw06591 Polypote
30	53	100.0	3391	AAW06590	AAw06590 Polypote
31	53	100.0	3391	AAE07987	AAe07987 Atenuate
32	53	100.0	3391	AAE07986	AAe07986 W1d-type
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34	49	92.5	39	ADM12582	Adm12582 M1-40/DEN
35	49	92.5	39	ADM12599	Adm12599 M1-40/DEN
36	48	92.5	48	ADM12588	Adm12588 P(95-114)
37	48	90.6	9	ADM12597	Adm12597 M2-40/DE
38	47	88.7	40	AAE17431	AAe17431 Dengue (D
39	47	88.7	48	AAE17437	AAe17437 (95-114)E
40	47	88.7	55	AAE17438	AAe17438 P(95-114)
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42	47	88.7	167	ADM37494	Adh37494 Dengue vi
43	47	88.7	167	ADM37501	Adh37501 Dengue vi
44	47	88.7	167	ADM37498	Adh37498 Dengue vi
45	47	88.7	167	ADM37492	Adh37492 Dengue vi
46	47	88.7	167	ADM37500	Adh37500 Dengue vi
47	47	88.7	661	AAH84901	AAh84901 Dengue-2
48	47	88.7	675	ADM37624	Adh37624 Dengue vi
49	47	88.7	675	ADM37519	Adh37519 Dengue vi
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51	47	88.7	675	ADM37616	Adh37616 Dengue vi
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54	47	88.7	675	ADM37604	Adh37604 Dengue vi
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58	47	88.7	675	ADM37615	Adh37615 Dengue vi
59	47	88.7	675	ADM37611	Adh37611 Dengue vi
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63	47	88.7	677	ADM37602	Adh37602 Dengue vi
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66	47	88.7	681	8	ADN37622	Adn37622 Dengue vi
67	47	88.7	684	8	ADR87180	Adr87180 Dengue vi
68	47	88.7	715	2	AAW065593	AAW065593 amino aci
69	47	88.7	774	8	ADC93320	Adc93320 DEN1 (Pue
70	47	88.7	775	8	ADC93318	Adc93318 DEN1 (Pue
71	47	88.7	798	2	AAW06592	AAW06592 Amino aci
72	47	88.7	3389	4	AAE07984	AAE07984 Dengue vi
73	47	88.7	3390	4	AAE07989	AAE07989 WILD-type
74	47	88.7	3390	4	AAE07990	AAE07990 Attenuate
75	47	88.7	3391	4	AAE07982	AAE07982 Dengue vi
76	47	88.7	3391	4	AAE07983	AAE07983 Dengue vi
77	47	88.7	3391	4	AAE07993	AAE07993 Dengue vi
78	47	88.7	3392	4	AAE07981	AAE07981 Attenuate
79	47	88.7	3392	4	AAE07980	AAE07980 WILD-type
80	47	88.7	3396	2	AAE43662	AAE43662 DEN1-5275
81	46	86.8	27	8	ADN11192	Adn11192 Peptide m
82	46	86.8	27	8	ADN11216	Adn11216 Peptide m
83	44	83.0	364	8	ADX92172	Adx92172 Plant ful
84	44	83.0	611	6	ABU22889	Abu22889 Protein e
85	44	83.0	9601	6	AAO29660	AAO29660 Paederus
86	43	81.1	27	8	ADN11218	Adn11218 Peptide m
87	43	81.1	27	8	ADN11194	Adn11194 Peptide m
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89	41	77.4	83	2	AAV60422	AAV60422 Human nor
90	41	77.4	167	8	ADN37495	Adn37495 Dengue vi
91	41	77.4	167	8	ADN37499	Adn37499 Dengue vi
92	41	77.4	635	2	AAW75412	AAW75412 Fusion pr
93	41	77.4	675	8	ADN37625	Adn37625 DEN-4/Den
94	41	77.4	675	8	ADN37627	Adn37627 DEN-4/Den
95	41	77.4	675	8	ADN37514	Adn37514 Dengue vi
96	41	77.4	675	8	ADN37520	Adn37520 Dengue vi
97	41	77.4	676	8	ADN37516	Adn37516 Dengue vi
98	41	77.4	677	8	ADN37605	Adn37605 Dengue vi
99	41	77.4	677	8	ADN37718	Adn37718 Dengue vi
100	41	77.4	678	8	ADN37720	Adn37720 Dengue vi
101	41	77.4	678	8	ADN37623	Adn37623 Dengue vi
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103	41	77.4	3387	4	AAE07991	AAE07991 WILD-type
104	41	77.4	3387	4	AAE07992	AAE07992 Attenuate
105	41	77.4	3387	6	AAE35313	AAE35313 Recombina
106	41	77.4	3387	6	AAE35312	AAE35312 Dengue vi
107	41	77.4	3391	4	AAE07985	AAE07985 Dengue vi
108	40	75.5	9	8	ADN11185	Adn11185 Peptide i
109	40	75.5	20	8	ADN11187	Adn11187 Peptide i
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112	40	75.5	21	8	ADN11203	Adn11203 Peptide m
113	40	75.5	21	8	ADN11221	Adn11221 Peptide m
114	40	75.5	22	8	ADN11201	Adn11201 Peptide m
115	40	75.5	22	8	ADN11235	Adn11235 Peptide m
116	40	75.5	24	8	ADN11223	Adn11223 Peptide m
117	40	75.5	24	8	ADN11205	Adn11205 Peptide m
118	40	75.5	27	8	ADN11196	Adn11196 Peptide m
119	40	75.5	27	8	ADN11195	Adn11195 Peptide m
120	40	75.5	27	8	ADN11220	Adn11220 Peptide m
121	40	75.5	27	8	ADN11191	Adn11191 Peptide m
122	40	75.5	27	8	ADN11215	Adn11215 Peptide m

123	40	75.5	27	8	ADN11219	Adn11219 Peptide m
124	40	75.5	31	8	ADN11225	Adn11225 Peptide m
125	40	75.5	31	8	ADN11207	Adn11207 Peptide m
126	40	75.5	39	5	AAE17434	AAE17434 Dengue vi
127	40	75.5	39	5	AAE17440	AAE17440 Dengue vi
128	40	75.5	40	8	ADN11182	Adn11182 Peptide i
129	40	75.5	149	4	AAE92543	AAE92543 C glutami
130	40	75.5	310	4	AAU35074	AAU35074 Enterococ
131	40	75.5	316	7	ADH87713	Adh87713 Enterococ
132	40	75.5	669	4	ABB69903	Abb69903 Drosophi1
133	39	73.6	85	7	ADC94455	Adc94455 E. faeciu
134	39	73.6	304	5	ABP30465	Abp30465 Streptoco
135	39	73.6	304	8	ADV82979	Adv82979 Streptoco
136	39	73.6	306	5	ABP27232	Abp27232 Streptoco
137	39	73.6	306	8	ADV88572	Adv88572 Streptoco
138	39	73.6	306	8	ADV80825	Adv80825 Streptoco
139	39	73.6	692	6	ABP57862	Abp57862 Plasmid P
140	38	71.7	60	4	AAU67387	AAU67387 Propionib
141	38	71.7	60	6	ABM63906	Abm63906 Propionib
142	38	71.7	132	4	ABG10849	Abg10849 Novel hum
143	38	71.7	167	9	ABM00905	Abm00905 Amino aci
144	38	71.7	183	5	AAE15961	AAE15961 Human 220
145	38	71.7	183	5	AAE15960	AAE15960 Human 631
146	38	71.7	198	4	AAU65420	AAU65420 Propionib
147	38	71.7	198	6	ABM61939	Abm61939 Propionib
148	38	71.7	217	6	ABJ18764	Abj18764 Pseudomon
149	38	71.7	230	7	ABO73461	AbO73461 Pseudomon
150	38	71.7	230	8	ADQ07629	AdQ07629 Amino aci

ALIGNMENTS

RESULT 1						
ADW12595						
ID	ADW12595	standard;	peptide;	9	AA.	
XX	XX					
AC	ADW12595;					
XX	XX					
DT	24-MAR-2005	(first entry)				
XX	XX					
DE	M32-40/DEN-2	mutant protein #1.				
XX	XX					
KW	Gene therapy; protein purification; virucide; cyrostatic; vaccine;					
KW	hemorrhage; bleeding; infection; flavivirus infection; neoplasm; cancer;					
PR	DEN; dengue; mutant; mutein.					
XX	XX					
OS	Dengue virus.					
XX	XX					
PN	US2004266987-A1.					
XX	XX					
PD	30-DEC-2004.					
XX	XX					
PF	30-JUN-2003; 2003US-00608029.					
XX	XX					
PR	30-JUN-2003; 2003US-00608029.					
XX	XX					

PA (INSP) INST PASTEUR.
 XX
 PI Despres P, Cateau A;
 XX
 DR WP1; 2005-047647/05.
 XX
 PT New isolated and purified ApoptoM peptide comprises 9 amino acids, useful
 PT as a vaccine for preventing or treating pathological conditions from non-
 PT specific febrile illnesses to severe hemorrhagic manifestations or
 PT encephalitic syndromes.
 XX
 PS Example 3; Fig 4; 30pp; English.
 XX
 CC The present invention relates to an isolated and purified ApoptoM
 CC peptide. The invention is useful as a vaccine for the prevention and
 CC treatment of pathological conditions from non-specific febrile illnesses
 CC to severe hemorrhagic manifestations, encephalitic syndromes and these
 CC pathological conditions are linked to Flavivirus infection or cancers.
 CC The invention is also useful in gene therapy. The present sequence is a
 CC M32-40/DEN (dengue)-2 mutant protein.
 XX
 SQ Sequence 9 AA;
 XX
 Query Match 100.0%; Score 53; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IETWILRHP 9
 1 IETWILRHP 9
 Db 1 IETWILRHP 9
 XX
 RESULT 2
 ADW12594
 ID ADW12594 standard; peptide; 21 AA.
 XX
 AC ADW12594;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE M20-40/DEN-2 mutant protein.
 XX
 KW Gene therapy; protein purification; virucide; cytostatic; vaccine;
 KW hemorrhage; bleeding; infection; flavivirus infection; neoplasm; cancer;
 KW DEN; dengue; mutant; mutein.
 XX
 OS Dengue virus.
 XX
 PN US2004266987-A1.
 XX
 PD 30-DEC-2004.
 XX
 PF 30-JUN-2003; 2003US-00608029.
 XX
 PR 30-JUN-2003; 2003US-00608029.
 XX
 PA (INSP) INST PASTEUR.

XX
 PI Despres P, Cateau A;
 XX
 DR WP1; 2005-047647/05.
 XX
 PT New isolated and purified ApoptoM peptide comprises 9 amino acids, useful
 PT as a vaccine for preventing or treating pathological conditions from non-
 PT specific febrile illnesses to severe hemorrhagic manifestations or
 PT encephalitic syndromes.
 XX
 PS Example 3; Fig 4; 30pp; English.
 XX
 CC The present invention relates to an isolated and purified ApoptoM
 CC peptide. The invention is useful as a vaccine for the prevention and
 CC treatment of pathological conditions from non-specific febrile illnesses
 CC to severe hemorrhagic manifestations, encephalitic syndromes and these
 CC pathological conditions are linked to Flavivirus infection or cancers.
 CC The invention is also useful in gene therapy. The present sequence is a
 CC M20-40/DEN (dengue)-2 mutant protein.
 XX
 SQ Sequence 21 AA;
 XX
 Query Match 100.0%; Score 53; DB 9; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IETWILRHP 9
 1 IETWILRHP 9
 Db 13 IETWILRHP 21
 XX
 RESULT 3
 ADW12593
 ID ADW12593 standard; peptide; 32 AA.
 XX
 AC ADW12593;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE M10-40/DEN-2 mutant protein.
 XX
 KW Gene therapy; protein purification; virucide; cytostatic; vaccine;
 KW hemorrhage; bleeding; infection; flavivirus infection; neoplasm; cancer;
 KW DEN; dengue; mutant; mutein.
 XX
 OS Dengue virus.
 XX
 PN US2004266987-A1.
 XX
 PD 30-DEC-2004.
 XX
 PF 30-JUN-2003; 2003US-00608029.
 XX
 PR 30-JUN-2003; 2003US-00608029.
 XX
 PA (INSP) INST PASTEUR.

P1 Despres P, Cateau A;
 XX
 DR WP1; 2005-047647/05.
 XX
 PT New isolated and purified ApoptoxM peptide comprises 9 amino acids, useful
 PT as a vaccine for preventing or treating pathological conditions from non-
 PT specific febrile illnesses to severe hemorrhagic manifestations or
 PT encephalitic syndromes.
 XX
 PS Example 3; Fig 4; 30pp; English.
 XX
 CC The present invention relates to an isolated and purified ApoptoxM
 CC peptide. The invention is useful as a vaccine for the prevention and
 CC treatment of pathological conditions from non-specific febrile illnesses
 CC to severe hemorrhagic manifestations, encephalitic syndromes and these
 CC pathological conditions are linked to Flavivirus infection or cancers.
 CC The invention is also useful in gene therapy. The present sequence is a
 CC M1-40/DEN (dengue)-2 mutant protein.
 XX
 SQ Sequence 32 AA:
 Query Match 100.0%; Score 53; DB 9; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IETWILRHP 9
 |||||
 DB 24 IETWILRHP 32
 RESULT 4
 ADM12576
 ID ADM12576 standard; peptide; 39 AA.
 XX
 AC ADM12576;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE M1-40/DEN-2 protein.
 XX
 KW Gene therapy; protein purification; virucide; cytostatic; vaccine;
 KW hemorrhage; bleeding; infection; flavivirus infection; neoplasm; cancer;
 KW DEN; dengue.
 XX
 OS Dengue virus.
 OS
 PN US2004266987-A1.
 PN
 XX
 PD 30-DEC-2004.
 PD
 XX
 PF 30-JUN-2003; 2003US-00608029.
 PF
 XX
 PR 30-JUN-2003; 2003US-00608029.
 PR
 XX
 PA (INSP) INST PASTEUR.
 PA
 XX
 P1 Despres P, Cateau A;

XX
 DR WP1; 2005-047647/05.
 XX
 PT New isolated and purified ApoptoxM peptide comprises 9 amino acids, useful
 PT as a vaccine for preventing or treating pathological conditions from non-
 PT specific febrile illnesses to severe hemorrhagic manifestations or
 PT encephalitic syndromes.
 XX
 PS Example 3; SEQ ID NO 23; 30pp; English.
 XX
 CC The present invention relates to an isolated and purified ApoptoxM
 CC peptide. The invention is useful as a vaccine for the prevention and
 CC treatment of pathological conditions from non-specific febrile illnesses
 CC to severe hemorrhagic manifestations, encephalitic syndromes and these
 CC pathological conditions are linked to Flavivirus infection or cancers.
 CC The invention is also useful in gene therapy. The present sequence is a
 CC M1-40/DEN (dengue)-2 protein.
 XX
 SQ Sequence 39 AA:
 Query Match 100.0%; Score 53; DB 9; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IETWILRHP 9
 |||||
 DB 31 IETWILRHP 39
 RESULT 5
 AAE17432
 ID AAE17432 standard; peptide; 40 AA.
 XX
 AC AAE17432;
 XX
 DT 29-AUG-2003 (revised)
 DT
 DT 18-APR-2002 (first entry)
 XX
 DE Dengue (DEN)-2 virus M ectodomain.
 XX
 KW Dengue virus; PRM glycoprotein; E glycoprotein; apoptosis; virucide;
 KW cancer; flavivirus infection; cytostatic; DEN-2 M ectodomain.
 XX
 OS Dengue virus; 2.
 OS
 PN WO200196376-A2.
 PN
 XX
 PD 20-DEC-2001.
 PD
 XX
 PF 18-JUN-2001; 2001WO-1B001570.
 PF
 XX
 PR 16-JUN-2000; 2000US-0212129P.
 PR
 XX
 PA (INSP) INST PASTEUR.
 PA
 XX
 P1 Despres P, Courageot M, Deibel V, Cateau A;

DR WP1: 2002-139706/18.

XX

XX Novel apoptosis inducing polypeptide fragments of Dengue virus-1 or 2 M

PT protein, useful for inducing apoptosis in a cell of a human patient

PT suffering from cancer or flavivirus infection.

XX

PS Claim 9; Fig 12; 45pp; English.

XX

CC The invention relates to pro-apoptotic fragments of the Dengue virus

CC (DEN) PRM and E glycoproteins, methods for screening molecules capable of

CC inducing apoptosis and methods of inducing apoptosis in a cell. The

CC invention particularly relates to DEN-1 M (a membrane protein anchored in

CC envelope surrounding the nucleocapsid of the virus) ectodomain sequence,

CC Den-1-C amino acid sequence and DEN-2 M ectodomain sequence. Sequences of

CC the invention are useful for inducing apoptosis in a cell of a patient

CC suffering from cancer or flavivirus infection. They are also useful for

CC screening molecules which inhibit apoptosis. The present sequence is DEN-2

CC virus M ectodomain. (Updated on 29-AUG-2003 to standardise OS field)

XX

SQ Sequence 40 AA:

Query Match 100.0%; Score 53; DB 5; Length 40;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9

DB 32 IETWILRHP 40

IIIIIIIIII

RESULT 6

ADW12578

ID ADW12578 standard; peptide; 40 AA.

XX

AC ADW12578;

XX

DT 24-MAR-2005 (first entry)

XX

DE M1-40/YF.17D (T34, 136, 137, H39) mutant protein.

XX

KW Gene therapy; protein purification; virucide; cytostatic; vaccine;

KW hemorrhage; bleeding; infection; flavivirus infection; neoplasm; cancer;

KW YF; yellow fever; mutant; muten.

XX

OS Yellow fever virus.

XX

PN US2004266987-A1.

XX

PD 30-DEC-2004.

XX

PF 30-JUN-2003; 2003US-00608029.

XX

PR 30-JUN-2003; 2003US-00608029.

XX

PA (INSP) INST PASTEUR.

XX

PI Despres P, Cateau A;

XX

XX WP1: 2005-047647/05.

XX

XX New isolated and purified Apoptom peptide comprises 9 amino acids, useful

PT as a vaccine for preventing or treating pathological conditions from non-

PT specific febrile illnesses to severe hemorrhagic manifestations or

PT encephalitic syndromes.

XX

PS Example 3; SEQ ID NO 25; 30pp; English.

XX

CC The present invention relates to an isolated and purified Apoptom

CC peptide. The invention is useful as a vaccine for the prevention and

CC treatment of pathological conditions from non-specific febrile illnesses

CC to severe hemorrhagic manifestations, encephalitic syndromes and these

CC pathological conditions are linked to Flavivirus infection or cancers.

CC The invention is also useful in gene therapy. The present sequence is a

CC M1-40/YF (yellow fever).17D (T34, 136, 137, H39) mutant protein.

XX

SQ Sequence 40 AA:

Query Match 100.0%; Score 53; DB 9; Length 40;

Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9

DB 32 IETWILRHP 40

IIIIIIIIII

RESULT 7

AAE17433

ID AAE17433 standard; protein; 48 AA.

XX

AC AAE17433;

XX

DT 18-APR-2002 (first entry)

XX

DE (95-114)EGFP(206-245)DEN-2 fusion protein.

XX

KW Dengue virus; PRM glycoprotein; E glycoprotein; apoptosis; virucide;

KW cancer; flavivirus infection; cytostatic; EGFP; DEN-2 protein;

KW enhanced green fluorescent protein; fusion protein; M ectodomain.

XX

OS Dengue virus; 2.

OS Dengue virus; 1.

OS Unidentified.

OS Chimeric.

XX

FH Key Location/Qualifiers

FT Misc-difference 13..44

XX

PN WO200196376-A2.

XX

PD 20-DEC-2001.

XX

PF 18-JUN-2001; 2001WO-1B001570.

XX	PR	16-JUN-2000; 2000US-0212129P.
XX	PA	(INSP) INST PASTEUR.
XX	P1	Despres P, Courageot M, Deubel V, Cateau A;
XX	P1	WPI: 2002-139706/18.
XX	DR	N-PSDB; MAD27335.
XX	PT	Novel apoptosis inducing polypeptide fragments of Dengue virus-1 or 2 M
XX	PT	protein, useful for inducing apoptosis in a cell of a human patient
XX	PT	suffering from cancer or flavivirus infection.
XX	PS	Claim 42; Fig 11; 45pp; English.
XX	CC	The invention relates to pro-apoptotic fragments of the Dengue virus
XX	CC	(DEN) pRNA and E glycoproteins, methods for screening molecules capable of
XX	CC	inducing apoptosis and methods of inducing apoptosis in a cell. The
XX	CC	invention particularly relates to DEN-1 M (a membrane protein anchored in
XX	CC	envelope surrounding the nucleocapsid of the virus) ectodomain sequences,
XX	CC	DEN-1-C amino acid sequence and DEN-2 M ectodomain sequence. Sequences of
XX	CC	the invention are useful for inducing apoptosis in a cell of a patient
XX	CC	suffering from cancer or flavivirus infection. They are also useful for
XX	CC	screening molecules which inhibit apoptosis. The present sequence is (95-
XX	CC	114)EGFP(206-243)DEN-2 fusion protein construct. This construct comprises
XX	CC	95-114 of the C-terminus of the C-protein of the DEN-1 virus strain BR/90
XX	CC	fused to the N-terminus of enhanced green fluorescent protein (EGFP) and
XX	CC	DEN-2 virus strain Jamaica M ectodomain (DEN-2 polypeptide) fused to the
XX	CC	C-terminus of the EGFP sequence
XX	SQ	Sequence 48 AA;
QY		1 IETWILRHP 9
Db		40 IETWILRHP 48
XX		100.0%; Score 53; DB 5; Length 48;
XX		Best Local Similarity 100.0%; Pred. No. 0.04;
XX		Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		RESULT 8
XX	ID	ADN37497
XX	AC	ADN37497 standard; protein; 167 AA.
XX	XX	ADN37497;
XX	DT	17-JUN-2004 (first entry)
XX	DE	Dengue virus C15/truncated p1M antigen fusion protein - SEQ ID 122.
XX	KW	virucide; Flavivirus; arboviruses group B; gene therapy; truncated p1M;
XX	XX	capid.
XX	OS	Dengue virus.

OS Dengue virus type 2.
 XX
 PN WO2003102166-A2.
 XX
 PD 11-DEC-2003.
 XX
 PF 26-FEB-2003; 2003WO-US005918.
 XX
 PR 26-FEB-2002; 2002US-0360030P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Apt D, Punnonen J, Brinkman AM;
 XX
 DR WPI; 2004-043106/04.
 XX
 PT New recombinant or synthetic polypeptides and polynucleotides useful for
 PT diagnosing, preventing or treating diseases associated with flaviviruses,
 PT including dengue viruses.
 XX
 PS Disclosure; SEQ ID NO 118; 409pp; English.
 XX
 CC The invention relates to a novel recombinant or synthetic polypeptide
 CC comprising an amino acid sequence that has at least about 90% sequence
 CC identity to any of the 20 fully defined amino acid sequences given in the
 CC specification. The polypeptide of the invention demonstrates virucide
 CC activity and may be useful for inducing an immune response to
 CC flaviviruses (arboviruses group B), including Dengue viruses, as well as
 CC in detecting and/or diagnosing the presence of antibodies against the
 CC Dengue virus serotypes in a sample and for gene therapy. The current
 CC sequence is that of a Dengue virus type 2 (DEN-2) C15/truncated prM
 CC antigen fusion protein of the invention which comprises the C-terminal 15
 CC amino acids of the capsid protein fused to a truncated form of the prM
 CC protein lacking the C-terminal 15 amino acids.
 XX
 SQ Sequence 171 AA;
 XX
 QY Query Match 100.0%; Score 53; DB 8; Length 171;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Db 1 IETWILRHP 9
 143 IETWILRHP 151
 |||||||||

RESULT 10
 ADN37496
 ID ADN37496 standard; protein; 171 AA.
 XX
 AC ADN37496;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Dengue virus C15/truncated prM antigen fusion protein - SEQ ID 121.
 XX
 KW virucide; flavivirus; arboviruses group B; gene therapy; truncated prM;

KW capsid.
 XX
 OS Dengue virus.
 XX
 PN WO2003102166-A2.
 XX
 PD 11-DEC-2003.
 XX
 PF 26-FEB-2003; 2003WO-US005918.
 XX
 PR 26-FEB-2002; 2002US-0360030P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Apt D, Punnonen J, Brinkman AM;
 XX
 DR WPI; 2004-043106/04.
 XX
 PT New recombinant or synthetic polypeptides and polynucleotides useful for
 PT diagnosing, preventing or treating diseases associated with flaviviruses,
 PT including dengue viruses.
 XX
 PS Disclosure; SEQ ID NO 121; 409pp; English.
 XX
 CC The invention relates to a novel recombinant or synthetic polypeptide
 CC comprising an amino acid sequence that has at least about 90% sequence
 CC identity to any of the 20 fully defined amino acid sequences given in the
 CC specification. The polypeptide of the invention demonstrates virucide
 CC activity and may be useful for inducing an immune response to
 CC flaviviruses (arboviruses group B), including Dengue viruses, as well as
 CC in detecting and/or diagnosing the presence of antibodies against the
 CC Dengue virus serotypes in a sample and for gene therapy. The current
 CC sequence is that of a Dengue virus C15/truncated prM antigen fusion
 CC protein of the invention which comprises the C-terminal 15 amino acids of
 CC the capsid protein fused to a truncated form of the prM protein lacking
 CC the C-terminal 15 amino acids.
 XX
 SQ Sequence 171 AA;
 XX
 QY Query Match 100.0%; Score 53; DB 8; Length 171;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Db 1 IETWILRHP 9
 143 IETWILRHP 151
 |||||||||

RESULT 11
 AAW75410
 ID AAW75410 standard; peptide; 635 AA.
 XX
 AC AAW75410;
 XX
 DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 02-MAR-1999 (first entry)

XX Fusion protein PD30 contains Dengue virus epitope.
 DE
 XX Dengue virus; fusion protein; P64K; Neisseria meningitidis; epitope;
 KW antibody; diagnosis; flavivirus; infection; vaccine.
 XX
 XX Dengue virus.
 OS Neisseria meningitidis.
 OS Chimeric.
 XX
 XX WO9831814-A1.
 PN
 XX 23-JUL-1998.
 PD
 XX 13-JAN-1998; 98WO-CU000001.
 PF
 XX 15-JAN-1997; 97CU-00000013.
 PR
 XX (CIGB-) CIGB CENT ING GENETICA & BIOTECNOLOGIA.
 PA (IPRM-) IPK INST MEDICINA TROPICAL KOURI PEDRO.
 XX
 XX Vazquez Ramudo S, Guzman tirado G, Guillen Nieto GE, Pardo lazo OL,
 P1 Chinae Santiago G, Perez Diaz AB, Pupo Antunez M, Rodriguez Roche R,
 P1 Reyes Acosta O, Garay Perez HE, Padron Palomares G, Alvarez Vera M;
 P1 Morier Diaz L, Perez Insueta O, Pelagrio Martinez De La Cotarri Pedro;
 XX WPI; 1998-41411/35.
 DR
 XX New peptide(s) and fusion proteins useful for diagnosis and treatment of
 PT flavivirus infection - contain cross-reactive epitopes from Dengue virus
 PT pre-W/M protein and can induce neutralising antibodies.
 PT
 XX Claim 7; Page 28-29; 64pp; Spanish.
 PS
 XX This protein represents a fusion protein comprising an M protein epitope
 CC from Dengue virus type 2 inserted into the P64K protein from Neisseria
 CC meningitidis. Synthetic peptides based on the Dengue virus epitope
 CC sequences (AAW75404-W75408) and fusion proteins can be used to raise
 CC antibodies. The peptides, protein and antibodies are all useful for
 CC diagnosis and treatment of flavivirus infection, e.g. in vaccines.
 CC (Updated on 25-MAR-2003 to correct P1 field.) (Updated on 17-OCT-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 635 AA;
 Query Match 100.0%; Score 53; DB 2; Length 635;
 Best Local Similarity 100.0%; Pred. No. 0.75;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 AC ADN37628;
 XX
 XX 17-JUN-2004 (first entry)
 DT
 XX Dengue virus C15/prM/E part codon-optimised antigen fusion protein 2.
 DE
 XX
 XX virucide; flavivirus; arboviruses group B; gene therapy; C15/prM/E;
 KW human codon-optimised; prM; envelope; capsid.
 XX
 XX Dengue virus.
 OS Synthetic.
 OS
 XX WO2003102166-A2.
 PN
 XX 11-DEC-2003.
 PD
 XX 26-FEB-2003; 2003WO-US005918.
 PF
 XX 26-FEB-2002; 2002US-0360030P.
 PR
 XX (MAXY-) MAXYGEN INC.
 PA Apt D, Punnonen J, Brinkman AM;
 P1 WPI; 2004-043106/04.
 P1
 XX N-PSDB; ADN37632.
 DR
 XX New recombinant or synthetic polypeptides and polynucleotides useful for
 PT diagnosing, preventing or treating diseases associated with flaviviruses,
 PT including dengue viruses.
 PT
 XX Example 28; SEQ ID NO 253; 409pp; English.
 PS
 XX The invention relates to a novel recombinant or synthetic polypeptide
 CC comprising an amino acid sequence that has at least about 90% sequence
 CC identity to any of the 20 fully defined amino acid sequences given in the
 CC specification. The polypeptide of the invention demonstrates virucide
 CC activity and may be useful for inducing an immune response to
 CC flaviviruses (arboviruses group B), including Dengue viruses, as well as
 CC in detecting and/or diagnosing the presence of antibodies against the
 CC Dengue virus serotypes in a sample and for gene therapy. The current
 CC sequence is that of the Dengue virus C15/prM/E partially human codon-
 CC optimised antigen fusion protein of the invention which comprises 15
 CC amino acids of the capsid (C) protein fused to the full-length partially
 CC codon-optimised prM protein and envelope (E) protein.
 XX
 SQ Sequence 675 AA;
 Query Match 100.0%; Score 53; DB 8; Length 675;
 Best Local Similarity 100.0%; Pred. No. 0.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 ADN37628
 ID ADN37628 standard; protein: 675 AA.

QY 1 IETWLRHP 9
 DB 139 IETWLRHP 147

RESULT 13

ADN37518

ID ADN37518 standard; protein; 675 AA.

XX

AC ADN37518;

XX

DT 17-JUN-2004 (first entry)

XX

DE Dengue virus C15/prM/E antigen fusion protein - SEQ ID 143.

XX

KW virucide; Flavivirus; arboviruses group B; gene therapy; C15/prM/E; prM; envelope; capsid.

XX

OS Dengue virus.

XX

PN W02003102166-A2.

XX

PD 11-DEC-2003.

XX

PF 26-FEB-2003; 2003WO-US005918.

XX

PR 26-FEB-2002; 2002US-0360030P.

XX

PA (MAXY-) MAXYGEN INC.

XX

P1 Apt D, Punnonen J, Brinkman AM;

XX

DR WPI; 2004-043106/04.

XX

PT New recombinant or synthetic polypeptides and polynucleotides useful for diagnosing, preventing or treating diseases associated with flaviviruses, including dengue viruses.

XX

PS Claim 40; SEQ ID NO 143; 409pp; English.

XX

CC The invention relates to a novel recombinant or synthetic polypeptide comprising an amino acid sequence that has at least about 90% sequence identity to any of the 20 fully defined amino acid sequences given in the CC specification. The polypeptide of the invention demonstrates virucide CC activity and may be useful for inducing an immune response to CC flaviviruses (arboviruses group B), including Dengue viruses, as well as CC in detecting and/or diagnosing the presence of antibodies against the CC Dengue virus serotypes in a sample and for gene therapy. The current CC sequence is that of the Dengue virus C15/prM/E antigen fusion protein of CC the invention which comprises 15 amino acids of the capsid (C) protein CC fused to the full-length prM protein and envelope (E) protein.

XX

SQ Sequence 675 AA;

Query Match 100.0%; Score 53; DB 8; Length 675;

Best Local Similarity 100.0%; Pred. No. 0.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9

DB 139 IETWILRHP 147

RESULT 14

ADN37612

ID ADN37612 standard; protein; 675 AA.

XX

AC ADN37612;

XX

DT 17-JUN-2004 (first entry)

XX

DE Dengue virus C15/prM/E antigen fusion protein - SEQ ID 237.

XX

KW virucide; Flavivirus; arboviruses group B; gene therapy; C15/prM/E; prM; envelope; capsid.

XX

OS Dengue virus.

XX

PN W02003102166-A2.

XX

PD 11-DEC-2003.

XX

PF 26-FEB-2003; 2003WO-US005918.

XX

PR 26-FEB-2002; 2002US-0360030P.

XX

PA (MAXY-) MAXYGEN INC.

XX

P1 Apt D, Punnonen J, Brinkman AM;

XX

DR WPI; 2004-043106/04.

XX

PT New recombinant or synthetic polypeptides and polynucleotides useful for diagnosing, preventing or treating diseases associated with flaviviruses, including dengue viruses.

XX

PS Claim 40; SEQ ID NO 237; 409pp; English.

XX

CC The invention relates to a novel recombinant or synthetic polypeptide comprising an amino acid sequence that has at least about 90% sequence identity to any of the 20 fully defined amino acid sequences given in the CC specification. The polypeptide of the invention demonstrates virucide CC activity and may be useful for inducing an immune response to CC flaviviruses (arboviruses group B), including Dengue viruses, as well as CC in detecting and/or diagnosing the presence of antibodies against the CC Dengue virus serotypes in a sample and for gene therapy. The current CC sequence is that of the Dengue virus C15/prM/E antigen fusion protein of CC the invention which comprises 15 amino acids of the capsid (C) protein CC fused to the full-length prM protein and envelope (E) protein.

XX

SQ Sequence 675 AA;

Query Match 100.0%; Score 53; DB 8; Length 675;

Best Local Similarity 100.0%; Pred. No. 0.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9

Db 139 1ETWILRHP 147

RESULT 15

ID AIN37626 standard; protein; 675 AA.

XX

AC AIN37626;

XX

DT 17-JUN-2004 (first entry)

XX

DE Dengue virus C15/prM/E part codon-optimised antigen fusion protein 1.

XX

KW virucide; Flavivirus; arboviruses group B; gene therapy; C15/prM/E;

XX

KW human codon-optimised; prM; envelope; capsid.

XX

OS Dengue virus.

OS Synthetic.

XX

PN WO2003102166-A2.

XX

PD 11-DEC-2003.

XX

PF 26-FEB-2003; 2003WO-US005918.

XX

PR 26-FEB-2002; 2002US-0360030P.

XX

PA (MAXY-) MAXYGEN INC.

XX

PI Apt D, Punnonen J, Brinkman AM;

XX

DR WPI: 2004-043106/04.

DR N-PSDB; AIN37630.

XX

PT New recombinant or synthetic polypeptides and polynucleotides useful for

PT diagnosing, preventing or treating diseases associated with flaviviruses,

PT including dengue viruses.

XX

PS Claim 40; SEQ ID NO 251; 409pp; English.

XX

CC The invention relates to a novel recombinant or synthetic polypeptide

CC comprising an amino acid sequence that has at least about 90% sequence

CC identity to any of the 20 fully defined amino acid sequences given in the

CC specification. The polypeptide of the invention demonstrates virucide

CC activity and may be useful for inducing an immune response to

CC flaviviruses (arboviruses group B), including Dengue viruses, as well as

CC in detecting and/or diagnosing the presence of antibodies against the

CC Dengue virus serotypes in a sample and for gene therapy. The current

CC sequence is that of the Dengue virus C15/prM/E partially human codon-

CC optimised antigen fusion protein of the invention which comprises 15

CC amino acids of the capsid (C) protein fused to the full-length partially

CC codon-optimised prM protein and envelope (E) protein.

XX

XX Sequence 675 AA;

Query Match 100.0%; Score 53; DB 8; Length 675;

Best Local Similarity 100.0%; Pred. No. 0.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 1ETWILRHP 9

DB 139 1ETWILRHP 147

RESULT 16

AAW75411

ID AAW75411 standard; peptide; 677 AA.

XX

AC AAW75411;

XX

DT 17-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 02-MAR-1999 (first entry)

XX

DE Fusion protein PD34 contains Dengue virus epitope.

XX

KW Dengue virus; fusion protein; P64K; Neisseria meningitidis; epitope;

KW antibody; diagnosis; Flavivirus; infection; vaccine.

XX

OS Dengue virus.

OS Neisseria meningitidis.

OS Chimeric.

XX

PN WO9831814-A1.

XX

PD 23-JUL-1998.

XX

PF 13-JAN-1998; 98WO-CU000001.

XX

PR 15-JAN-1997; 97CU-00000013.

XX

PA (CIGB-) CIGB CENT ING GENETICA & BIOTECNOLOGIA.

PA (IPRM-) IPRM INST MEDICINA TROPICAL KOURI PEDRO.

XX

PI Vazquez Ramado S, Guzman Tirado G, Guillen Nieto GE, Pardo Iazo OI;

PI Chinaa Santiago G, Perez Diaz AB, Pupo Antunes M, Rodriguez Roche R;

PI Reyes Acosta O, Garey Perez HE, Padron Palomares G, Alvarez Vera M;

PI Morier Diaz L, Perez Insulza O, Pelagrinio Martinez De La Cotterri Pedro;

XX

DR WPI: 1998-41411/35.

XX

PT New peptide(s) and fusion proteins useful for diagnosis and treatment of

PT flavivirus infection - contain cross-reactive epitopes from Dengue virus

PT pre-M/E protein and can induce neutralising antibodies.

XX

PS Claim 7; Page 30-32; 64pp; Spanish.

XX

CC This protein represents a fusion protein comprising an M protein epitope

CC from Dengue virus type 4 inserted into the P64K protein from Neisseria

CC meningitidis. Synthetic peptides based on the Dengue virus epitope

CC sequences (AAW75404-W75408) and fusion proteins can be used to raise

CC antibodies. The peptides, protein and antibodies are all useful for

CC diagnosis and treatment of Flavivirus infection, e.g. in vaccines.

CC (Updated on 25-MAR-2003 to correct PI field.) (Updated on 17-OCT-2003 to

CC sequence is that of the Dengue virus type 2 (DEN-2) Den-2C15/prM/E
 CC antigen fusion protein of the invention which comprises 15 amino acids of
 CC the capsid (C) protein fused to the full-length prM protein and envelope
 CC (E) protein.
 XX
 XX
 SQ Sequence 681 AA;

Query Match 100.0%; Score 53; DB 8; Length 681;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRRP 9
 |||||
 Db 143 IETWILRRP 151

RESULT 19
 ADN37517
 ID ADN37517 standard; protein; 681 AA.
 XX
 AC ADN37517;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Dengue virus C15/prM/E antigen fusion protein - SEQ ID 142.
 XX
 KW virucide; Flavivirus; arboviruses group B; gene therapy; C15/prM/E; prM;
 KW envelope; capsid.
 XX
 OS Dengue virus.
 XX
 PN WO2003102166-A2.
 XX
 PD 11-DEC-2003.
 XX
 PF 26-FEB-2003; 2003WO-US005918.
 XX
 PR 26-FEB-2002; 2002US-0360030P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Apt D, Punnonen J, Brinkman AM;
 XX
 DR WPI; 2004-043106/04.
 XX
 PT New recombinant or synthetic polypeptides and polynucleotides useful for
 PT diagnosing, preventing or treating diseases associated with flaviviruses,
 PT including dengue viruses.
 XX
 PS Claim 40; SEQ ID NO 142; 409pp; English.
 XX
 CC The invention relates to a novel recombinant or synthetic polypeptide
 CC comprising an amino acid sequence that has at least about 90% sequence
 CC identity to any of the 20 fully defined amino acid sequences given in the
 CC specification. The polypeptide of the invention demonstrates virucide
 CC activity and may be useful for inducing an immune response to
 CC flaviviruses (arboviruses group B), including Dengue viruses, as well as

CC in detecting and/or diagnosing the presence of antibodies against the
 CC Dengue virus serotypes in a sample and for gene therapy. The current
 CC sequence is that of the Dengue virus C15/prM/E antigen fusion protein of
 CC the invention which comprises 15 amino acids of the capsid (C) protein
 CC fused to the full-length prM protein and envelope (E) protein.
 XX
 XX
 SQ Sequence 681 AA;

Query Match 100.0%; Score 53; DB 8; Length 681;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRRP 9
 |||||
 Db 143 IETWILRRP 151

RESULT 20
 ABP57874
 ID ABP57874 standard; protein; 685 AA.
 XX
 AC ABP57874;
 XX
 DT 07-FEB-2003 (first entry)
 XX
 DE Plasmid pCBD2-14-6 containing dengue-2 virus prM and E.
 XX
 KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
 KW pCBD2-14-6; dengue virus; DEN-2.
 XX
 OS Unidentified.
 OS Dengue-2 virus.
 OS Chimeric.
 XX
 PN WO200281754-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 04-APR-2002; 2002WO-US010764.
 XX
 PR 04-APR-2001; 2001US-00826115.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Chang GJ;
 XX
 DR WPI; 2003-058572/05.
 DR N-PSDB; ABV77547.
 XX
 PT Novel isolated nucleic acid useful as vaccine for preventing flavivirus
 PT infection, comprises transcriptional unit encoding signal sequence of one
 PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.
 XX
 PS Example 20; Page 157-158; 174pp; English.
 XX
 CC The invention relates to a novel nucleic acid comprising a
 CC transcriptional unit encoding a signal sequence of a structural protein

CC of a first flavivirus and an immunogenic flavivirus antigen of a second
 CC flavivirus, where the transcriptional unit directs the synthesis of the
 CC antigen. The polynucleotide of the invention has virucide activity, and
 CC acts as a vaccine. A composition of the invention is useful for
 CC immunising a subject against infection by a flavivirus. The
 CC polynucleotide is useful as a vaccine for preventing flavivirus
 CC infection. The sequence represents plasmid pCBSD2-14-6, which contains
 CC dengue-2 virus (DEN-2) prM and E proteins

XX
 SQ Sequence 685 AA;

Query Match 100.0%; Score 53; DB 6; Length 685;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
 |||||||||
 Db 147 IETWILRHP 155

RESULT 21
 ABP57876
 ID ABP57876 standard; protein; 685 AA.
 XX
 AC ABP57876;
 XX
 DT 07-FEB-2003 (first entry)
 XX
 DE Plasmid pCBSD2-2J-2-9-1 protein product.
 XX
 KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
 KW pCBSD2-2J-2-9-1; Japanese encephalitis virus; dengue-2 virus; DEN-2.
 XX
 OS Unidentified.
 OS Synthetic.
 XX
 FN W0200281754-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 04-APR-2002; 2002WO-US010764.
 XX
 PR 04-APR-2001; 2001US-00826115.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 P1 Chang GJ;
 XX
 DR WP1; 2003-058572/05.
 DR N-PSDB; ABV77549.
 XX
 PT Novel isolated nucleic acid useful as vaccine for preventing flavivirus
 PT infection, comprises transcriptional unit encoding signal sequence of one
 PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.
 XX
 PS Example 20; Page 168-169; 174pp; English.
 XX

CC The invention relates to a novel nucleic acid comprising a
 CC transcriptional unit encoding a signal sequence of a structural protein
 CC of a first flavivirus and an immunogenic flavivirus antigen of a second
 CC flavivirus, where the transcriptional unit directs the synthesis of the
 CC antigen. The polynucleotide of the invention has virucide activity, and
 CC acts as a vaccine. A composition of the invention is useful for
 CC immunising a subject against infection by a flavivirus. The
 CC polynucleotide is useful as a vaccine for preventing flavivirus
 CC infection. The sequence represents plasmid pCBSD2-2J-2-9-1, which
 CC contains dengue-2 virus (DEN-2) prM, M and E, and Japanese encephalitis
 CC virus E proteins

XX
 SQ Sequence 685 AA;

Query Match 100.0%; Score 53; DB 6; Length 685;
 Best Local Similarity 100.0%; Pred. No. 0.82;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
 |||||||||
 Db 147 IETWILRHP 155

RESULT 22
 ABP57875
 ID ABP57875 standard; protein; 685 AA.
 XX
 AC ABP57875;
 XX
 DT 07-FEB-2003 (first entry)
 XX
 DE Plasmid pCBSD2-1J-4-3 protein product.
 XX
 KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
 KW pCBSD2-1J-4-3; Japanese encephalitis virus; dengue-2 virus; DEN-2.
 XX
 OS Unidentified.
 OS Synthetic.
 XX
 FN W0200281754-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 04-APR-2002; 2002WO-US010764.
 XX
 PR 04-APR-2001; 2001US-00826115.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 P1 Chang GJ;
 XX
 DR WP1; 2003-058572/05.
 DR N-PSDB; ABV77548.
 XX
 PT Novel isolated nucleic acid useful as vaccine for preventing flavivirus
 PT infection, comprises transcriptional unit encoding signal sequence of one
 PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.
 XX

```

XX PS Example 20; Page 162-164; 174pp; English.
XX CC The invention relates to a novel nucleic acid comprising a
CC CC transcriptional unit encoding a signal sequence of a structural protein
CC of a first flavivirus and an immunogenic flavivirus antigen of a second
CC flavivirus, where the transcriptional unit directs the synthesis of the
CC antigen. The polynucleotide of the invention has virucide activity, and
CC acts as a vaccine. A composition of the invention is useful for
CC immunising a subject against infection by a flavivirus. The
CC polynucleotide is useful as a vaccine for preventing flavivirus
CC infection. The sequence represents plasmid PC9D2-1J-4-3, which contains
CC dengue-2 virus (DEN-2) pRfl, M and E, and Japanese encephalitis virus E
CC proteins
XX CC
SQ Sequence 685 AA;

Query Match      100.0%; Score 53; DB 6; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IETWLRHP 9
        |||||
DB      147 IETWLRHP 155

RESULT 23
AAW09409
ID AAW09409 standard; protein; 1127 AA.
XX AC
XX AAW09409;
XX AC
XX 17-OCT-2003 (revised)
DT 19-MAY-1997 (first entry)
XX DE
DE Dengue virus serotype 2 PR159/S1 polypeptide.
XX KW
KW DEN-2; flavivirus; envelope protein; immunisation; vaccine.
XX OS
OS Dengue virus; serotype 2.
XX FH
FH Key Location/Qualifiers
FT Region 1..114
FT /label= Capsid
FT Region 115..205
FT /label= Pre-membrane
FT Region 206..280
FT /label= Membrane
FT Region 281..775
FT /label= Envelope
FT Domain 296..395
FT /label= Domain-B
FT Misc-difference 588
FT /note= "amino acid residue 598 (Val) is Ile in wild-type
FT PR159"
FT 776..1127
FT Region
FT /label= NS1

```

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XX PN WO9637221-A1.
XX PD 28-NOV-1996.
XX PF 24-MAY-1996; 96WO-US007627.
XX PR 24-MAY-1995; 95US-00448734..
PR 07-JUN-1995; 95US-00488807.
PR 10-JUL-1995; 95US-00500469.
XX PA (HAWA-) HAWA11 BIOTECHNOLOGY GROUP INC.
XX PI Ivy JM, Nakano E, Clements D;
XX DR WPI; 1997-020938/02.
XX DR N-PSDB; AAT47666.
XX PT Subunit vaccine against flavivirus infection - contg. recombinant
PT envelope protein in secretable form, used for immunising against
PT flavivirus infection.
XX PS
XX Example 1; Fig 3A-D; 121pp; English.
XX CC A polypeptide (AAW09409) comprises the capsid, pre-membrane, envelope and
CC NS1 proteins of dengue virus serotype 2 (DEN-2) variant PR159/S1. A
CC conservative mutation in the envelope protein may be involved in the
CC attenuation of this small-plaque, temp.-sensitive variant. Portions of
CC the envelope protein, esp. domain B, can be expressed in eukaryotic hosts
CC (see also AAW09410 and AAW09427-28) transfected with vectors
CC incorporating DEN-2 S1 cDNA (see also AAT47666). These polypeptides can
CC be used in novel subunit vaccines against viral infection, to raise
CC antibodies useful for passive immunisation, and for diagnosis of
CC infection. (Updated on 17-OCT-2003 to standardise OS field)
XX SQ Sequence 1127 AA;

Query Match      100.0%; Score 53; DB 2; Length 1127;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IETWLRHP 9
        |||||
DB      237 IETWLRHP 245

RESULT 24
AAV05522
ID AAV05522 standard; protein; 1127 AA.
XX AC
XX AAV05522;
XX AC
XX 17-OCT-2003 (revised)
DT 05-JUL-1999 (first entry)
XX DE
DE Dengue virus serotype 2 PR159/S1 viral capsid, pRfl, E, NS1.
XX

```

KW Flavivirus; envelope protein; vaccine; infection; diagnosis.
 XX Dengue virus; serotype 2.
 OS
 XX
 FH Key Location/Qualifiers
 FT Protein 1..114
 FT /label= Capsid
 FT Protein 115..205
 FT /label= PreMembrane
 FT Protein 206..280
 FT /label= Membrane
 FT Protein 280..1127
 FT /label= Envelope
 XX
 PN WO9906068-A2.
 XX
 PD 11-FEB-1999.
 XX
 PF 27-JUL-1998; 98WO-US015447.
 XX
 PR 31-JUL-1997; 97US-00904227.
 XX
 PA (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
 XX
 PI Ivy JM, Peters ID, Collier BG, McDonnell M, Harada KE;
 XX
 DR WPI; 1999-153454/13.
 DR N-PSDB; AAX25114.
 XX
 XX
 PT Recombinant dimeric flaviviral envelope vaccine - comprising a dimeric
 PT 80% protein, useful for protecting against flavivirus, especially dengue
 PT virus infections.
 XX
 XX
 PS Example 1; Fig 3A-D; 60pp; English.
 XX
 CC This sequence is composed of the capsid, prM, envelope (E) and NS1
 CC proteins of serotype 2 dengue virus DEN-2 strain PR159/SI. A vaccine for
 CC protecting against flavivirus infection comprises a dimeric 80% E protein
 CC that has been secreted as a recombinant protein from a eukaryotic cell.
 CC 80% E indicates a C-terminally truncated flavivirus E protein. The
 CC dimeric truncated E is formed: (1) by directly linking 2 tandem copies of
 CC 80% E via a flexible tether; (2) via the formation of 2 leucine zipper helices
 CC domain through the homodimeric association of 2 leucine zipper helices
 CC each fused to the C-terminus of an 80% E molecule; or (3) via the
 CC formation of a non-covalently associated four-helix bundle domain formed
 CC upon association of two helix-turn-helix moieties attached to the C-
 CC termini of an 80% E molecule. Dimeric truncated DEN-2 E proteins are
 CC efficiently secreted by recombinant cells, are easier to purify than
 CC intracellular proteins, and generate a high titer neutralising antibody
 CC response. The method is generally applicable to flaviviruses, in
 CC particular dengue viruses such as DEN-2, where 80% E comprises amino
 CC acids 1-395 of DEN-2 E. The products can also be used for diagnosis of
 CC infection. (Updated on 17-OCT-2003 to standardise OS field)
 CC
 XX
 XX Sequence 1127 AA;
 SQ
 Query Match 100.0%; Score 53; DB 2; Length 1127;

Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IETWILRHP 9
 DB 237 IETWILRHP 245
 RESULT 25
 ADL98086
 ID ADL98086 standard; protein; 1127 AA.
 XX
 AC ADL98086;
 XX
 PI 18-NOV-2004 (first entry)
 XX
 DE Dengue virus, DEN-2, capsid/membrane/envelope/NS1 proteins.
 XX
 KW Dengue virus; DEN-2; Envelope protein; 80% E; membrane protein;
 KW capsid protein; NS1 protein; Dengue haemorrhagic fever; DHF;
 KW Dengue shock syndrome; DSS; flavivirus; vaccine.
 XX
 OS Dengue virus type 2; strain PR159/SI.
 XX
 PN US2003175304-A1.
 XX
 PD 18-SEP-2003.
 XX
 PF 20-SEP-2002; 2002US-00247960.
 XX
 PR 31-JUL-1997; 97US-00904227.
 PR 18-AUG-1999; 99US-00376463.
 XX
 XX (PETE/) PETERS I D.
 PA (COLL/) COLLIER B G.
 PA (MCDON/) MCDONNELL M.
 PA (IVYJ/) IVY J M.
 PA (HARAV/) HARADA K.
 XX
 PI Peters ID, Collier BG, McDonnell M, Ivy JM, Harada K;
 XX
 DR WPI; 2003-898503/82.
 DR N-PSDB; ADL98085.
 XX
 XX Vaccine useful for protection against dengue virus infection, comprises a
 PT dimeric 80% envelope, which has been secreted as a recombinantly produced
 PT protein from Drosophila Schneider cells.
 XX
 PS Example 1; Fig 3; 31pp; English.
 XX
 CC The invention relates to a vaccine for protection against flavivirus
 CC infection comprising a dimeric 80% envelope (E), which has been secreted
 CC as a recombinantly produced protein from Drosophila Schneider cells and
 CC which represents the N-terminal 80% portion of the protein from residue 1
 CC -395. Also included are a method for protecting a subject against a
 CC flavivirus, an immunogenic polypeptide comprising a dimeric 80% E, an
 CC immunogenic composition for protection against flavivirus infection

comprising the immunogenic polypeptide and a carrier, an immunodiagnostic kit for detecting Flavivirus comprising the immunogenic polypeptide, a vector host recombinant DNA expression system, a DNA sequence encoding the immunogenic polypeptide and an immunodiagnostic kit for detecting Flavivirus in a test subject. The dimeric 80kE products are envelope proteins of serotypes comprising DEN-1, DEN-2, DEN-3 or DEN-4. The Flavivirus is a dengue virus. The 80kE protein is produced as a dimer by incorporating 2 different kinds of leucine zipper peptides or incorporating a helix-turn-helix peptide, to encourage dimerisation. The vaccine is useful for protection against dengue virus infection (e.g. Dengue haemorrhagic fever, DHF, and Dengue shock syndrome, DSS). The present sequence is encoded by the partial genomic sequence of the DEN-2 strain PR159/SI virus, and represents the capsid, membrane, envelope and NS1 proteins.

XX Sequence 1127 AA;

Query Match 100.0%; Score 53; DB 7; Length 1127;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
 |||||

Db 237 IETWILRHP 245

RESULT 26
 ADQ28716
 ID ADQ28716 standard; protein; 1127 AA.
 XX
 AC ADQ28716;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Dengue virus viral capsid, prM, E and NS1 gene polypeptide.
 XX
 KW virucide; vaccine; Flavivirus; dimeric 80kE; Drosophila Schneider cell;
 KW immunogenic composition; multivalent immunodiagnostic; dengue virus;
 KW viral capsid; prM gene; E gene; NS1 gene.
 XX
 OS Dengue virus.
 XX
 PN US6749857-B1.
 XX
 PD 15-JUN-2004.
 XX
 PF 18-AUG-1999; 99US-00376463.
 XX
 PR 31-JUL-1997; 97US-00904227.
 XX
 PA (HAWAII) HAWAII BIOTECHNOLOGY GROUP INC.
 XX
 PI Peters ID, Collier BG, McDonnell M, Ivy JM, Harada K;
 XX WPI; 2004-438725/41.
 DR N-PSDB; ADQ28715.
 XX

New vaccines for preventing or diagnosing infections caused by dengue virus comprises a therapeutic amount of a dimeric 80kE protein secreted from Drosophila Schneider cells.

XX Example 1; SEQ ID NO 3; 47bp; English.

PS The invention describes a vaccine that generates a protective, neutralising antibody response to a Flavivirus in a murine host. The vaccine comprises a therapeutic amount of a dimeric 80kE, the dimeric 80kE having been secreted as a recombinantly produced protein from Drosophila Schneider cells, and where 80kE represents the N-terminal 80k portion of the protein from residues 1-395. Also described are: an immunogenic polypeptide comprising the dimeric 80kE cited above; an immunogenic composition that generates a protective, neutralising antibody response to a Flavivirus in a murine host, comprising the above immunogenic polypeptide and a physiological carrier; a multivalent immunodiagnostic for the detection of Flavivirus, comprising at least 2 of the above immunogenic polypeptides of at least 2 flaviviral serotypes; and an immunodiagnostic kit for the detection of Flavivirus in a test subject, comprising the above immunogenic or multivalent immunodiagnostic polypeptide, a suitable support phase coated with dimeric 80kE, and labeled antibodies immunoreactive to antibodies from the test subject. The composition is useful for preventing or diagnosing infections caused by dengue virus. This is the amino acid sequence of the polypeptide encoded by Dengue virus gene viral capsid, prM, E and NS1 genes for Dengue virus strain PR159/SI used as the source of DEN-2 genes for the invention.

XX Sequence 1127 AA;

Query Match 100.0%; Score 53; DB 8; Length 1127;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
 |||||

Db 237 IETWILRHP 245

RESULT 27
 AAE35314
 ID AAE35314 standard; protein; 3388 AA.
 XX
 AC AAE35314;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Dengue virus type 2 strain rDEN2/4delta30 protein.
 XX
 KW Attenuation; growth; vaccine; infection; Dengue virus type 4.
 XX
 OS Dengue virus.
 XX
 PN WO200295075-A1.
 XX
 PD 28-NOV-2002.
 XX

PF	22-MAY-2002; 2002WO-US016308.	FT	/label= prM
XX		FT	183
PR	22-MAY-2001; 2001US-0293049P.	FT	/label= N-glycosylated
XX		FT	206. .280
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	FT	/label= M
PA	(BLAN/) BLANEY J E.	FT	281. .775
XX		FT	/label= E
PI	Whitehead SS, Murphy BR, Hanley KA;	FT	347
XX		FT	/label= N-glycosylated
DR	WPI; 2003-120809/11.	FT	433
DR	N-PSDB; AAD53912.	FT	/label= N-glycosylated
XX		FT	776. .1127
XX		FT	/label= NS1
PT	New mutated flavivirus, useful for fine tuning the attenuation and growth	FT	905
PT	characteristics of dengue virus vaccines for the prevention and/or	FT	/label= N-glycosylated
PT	treatment of dengue virus infection.	FT	982
XX		FT	/label= N-glycosylated
XX		FT	1128. .1345
PS	Disclosure; Page 133-134; 246pp; English.	FT	/label= NS2A
XX		FT	1134
CC	The present invention relates to novel mutated flaviviruses comprising a	FT	/label= N-glycosylated
CC	phenotype in which the viral genome is modified by introduction of a	FT	1174
CC	mutation, singly or in combination, taken from mutations from recombinant	FT	/label= N-glycosylated
CC	virus bearing Vero adaptation mutations, putative Vero cell adaptation	FT	1329
CC	mutations of dengue type 4 virus (DENV4) or mutations known to attenuate	FT	/label= N-glycosylated
CC	dengue type 4 virus. The methods and compositions of the invention are	FT	1346. .1474
CC	useful for fine tuning the attenuation and growth characteristics of	FT	/label= NS2B
CC	dengue virus vaccines for the prevention and/or treatment of dengue virus	FT	1369
CC	infection. The present sequence is Dengue virus type 4 strain	FT	/label= N-glycosylated
CC	DENV2/delta30 protein	FT	1475. .2093
XX		FT	/label= NS3
SQ	Sequence 3388 AA;	FT	2094. .2243
		FT	/label= ns4a
	Query Match 100.0%; Score 53; DB 6; Length 3388;	FT	2244. .2492
	Best Local Similarity 100.0%; Pred. No. 5;	FT	/label= NS4B
	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FT	2301
OY	1 IETWILRHP 9	FT	2305
		FT	/label= N-glycosylated
Db	237 IETWILRHP 245	FT	2457
		FT	/label= N-glycosylated
		FT	2485
		FT	/label= N-glycosylated
		FT	2493. .3391
		FT	/label= NS5
		FT	2644
		FT	/label= N-glycosylated
		FT	2665
		FT	/label= N-glycosylated
		FT	2704
		FT	/label= N-glycosylated
		FT	2714
		FT	/label= N-glycosylated
		XX	FR265413-A.
		XX	

PD 10-MAY-1991.
 XX
 PF 09-NOV-1989; 89FR-00914724.
 XX
 PR 09-NOV-1989; 89FR-00014724.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Vincent D;
 XX
 DR WPI; 1991-225002/31.
 DR N-PSDB; AAQ12787.
 XX
 PT Detection and identification of Flaviviridae in biological sample - by
 amplifying consensus sequence then hybridisation opt. followed by typing,
 e.g. sequencing amplified prod.
 PT
 XX
 PS Disclosure; Fig 3; 24pp; French.
 XX
 CC The dengue 2 virus is an example of a member of the Flaviviridae which
 can be identified using the probe pair of the invention. A species-
 CC specific sequence can be amplified using the claimed oligonucleotides as
 CC primers in a PCR reaction (see AAQ12788 and AAQ12789). Other viruses
 CC which can be identified include Japanese encephalitis virus and yellow
 CC fever virus. All the dengue 2 virus proteins are encoded from an
 CC uninterrupted genomic sequence. (Updated on 25-MAR-2003 to correct PR
 CC field.)
 CC
 XX
 SQ Sequence 3391 AA;
 Query Match 100.0%; Score 53; DB 2; Length 3391;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IETWLRHP 9
 |||||||||
 DB 237 IETWLRHP 245
 RESULT 29
 AA06591
 ID AA06591 standard; protein; 3391 AA.
 XX
 AC AA06591;
 XX
 DT 27-AUG-2003 (revised)
 DT 12-SEP-1997 (first entry)
 XX
 DE Polypeptide of attenuated DEN-2 virus, strain 16681, PDK-53.
 XX
 KW Dengue 2 virus; polypeptide; capsid; pM; M; E; NS1; NS2A; NS2B; NS3;
 NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
 KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
 dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
 DHF; DSS.
 KW
 XX
 OS Dengue virus type 2 (strain 16681).
 XX
 FH Key Location/Qualifiers
 FT Protein 2..114
 FT /label= Capsid_protein
 FT Protein 115..205
 FT /label= pM
 FT Modified-site 183
 FT /note= "N-linked glycosylation site, encoded by NAC"
 FT Protein 206..280
 FT /label= M
 FT Protein 281..775
 FT /label= E
 FT Modified-site 347
 FT /note= "N-linked glycosylation site, encoded by NAC"
 FT Modified-site 433
 FT /note= "N-linked glycosylation site, encoded by NAT"
 FT Protein 776..1127
 FT /label= NS1
 FT Modified-site 905
 FT /note= "N-linked glycosylation site, encoded by NAC"
 FT Modified-site 982
 FT /note= "N-linked glycosylation site, encoded by NAT"
 FT Protein 1128..1345
 FT /label= NS2A
 FT Protein 1346..1475
 FT /label= NS2B
 FT Protein 1476..2093
 FT /label= NS3
 FT Protein 2094..2242
 FT /label= NS4A
 FT Protein 2243..2491
 FT /label= NS4B
 FT Protein 2492..3391
 FT /label= NS5
 FT Misc-difference 3038
 FT /note= "Encoded by KKA"
 XX
 PN W09640933-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US009209.
 XX
 PR 07-JUN-1995; 95US-00483292.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (UYMA-) UNIV MAHIDOL AT SALAYA.
 XX
 PI Bhamarapavati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
 PI Kliney R, Trent DW;
 DR WPI; 1997-052330/05.
 DR N-PSDB; AAT49304.
 XX
 KW PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
 PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
 PT quadravalent vaccine for protecting against Dengue virus infection.

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XX Claim 27, Page 122-136; 261pp; English.
PS
CC This sequence represents the polypeptide from attenuated Dengue 2 virus,
CC strain 16681. The attenuated virus is designated PDK-53. The poly-
CC protein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B
CC and NS5 proteins. A clone of this wildtype viral sequence, PDK-53, may be
CC used in the production of a quadravalent vaccine which provides immunity
CC against all four serotypes of dengue virus. The vaccine also comprises a
CC chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-
CC 2/4 virus. The new quadravalent vaccines are used to protect against
CC infection by all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and
CC DEN-4, which can lead to dengue fever or fatal dengue haemorrhagic
CC fever/dengue shock syndrome (DHF/DSS). Host cells are used to produce the
CC recombinant protein products of the DNA constructs which are used in the
CC vaccines. (Updated on 27-AUG-2003 to correct 05 field.)
XX
SQ Sequence 3391 AA;
Query Match 100.0%; Score 53; DB 2; Length 3391;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IETWLRHP 9
Db 237 IETWLRHP 245
|||||||
RESULT 30
AAW06590
ID AAW06590 standard; protein; 3391 AA.
XX
AC AAW06590;
XX
DT 27-AUG-2003 (revised)
DT 11-SEP-1997 (first entry)
XX
DE Polypeptide of DEN-2 virus, strain 16681.
XX
KW Dengue 2 virus; polypeptide; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW DHF; DSS.
XX
OS Dengue virus type 2 (strain 16681).
XX
FH Key Location/Qualifiers
FT Protein 2..114
FT Protein /label=Capsid_protein
FT Protein 115..205
FT Protein /label=prM
FT Modified-site 183
FT /note="N-linked glycosylation site"
FT Protein 206..280
FT Protein /label=M
FT Protein 281..775

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FT FT /label=E
FT Modified-site 347
FT /note="N-linked glycosylation site"
FT Modified-site 433
FT /note="N-linked glycosylation site"
FT Protein 776..1127
FT /label=NS1
FT Modified-site 905
FT /note="N-linked glycosylation site"
FT Modified-site 982
FT /note="N-linked glycosylation site"
FT Protein 1128..1345
FT /label=NS2A
FT Protein 1346..1475
FT /label=NS2B
FT Protein 1476..2093
FT /label=NS3
FT Protein 2094..2242
FT /label=NS4A
FT Protein 2243..2491
FT /label=NS4B
FT Protein 2492..3391
FT /label=NS5
FT Misc-difference 3038
FT /note="Encoded by KKA"
XX
PN W09640933-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96MO-US009209.
XX
PR 07-JUN-1995; 95US-00483292.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
PI Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
PI Kinney R, Trent DW;
XX
DR WP1; 1997-052330/05.
DR N-PSDB; AAT49303.
XX
PT PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
PT quadravalent vaccine for protecting against Dengue virus infection.
XX
PS Claim 23; Page 107-121; 261pp; English.
XX
CC This sequence represents the polypeptide from Dengue 2 virus, strain
CC 16681. The polypeptide comprises the capsid, prM, M, E, NS1, NS2A, NS2B,
CC NS3, NS4A, NS4B and NS5 proteins. A clone of this wildtype viral
CC sequence, PDK-53, may be used in the production of a quadravalent vaccine
CC which provides immunity against all four serotypes of dengue virus. The
CC vaccine also comprises a chimeric DEN-2/1 virus, a chimeric DEN-2/3
CC virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are
CC used to protect against infection by all four serotypes of dengue virus,

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CC DEN-1, DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal
CC dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are
CC used to produce the recombinant protein products of the DNA constructs
CC which are used in the vaccines. (Updated on 27-AUG-2003 to correct OS
CC field.)
XX

SQ Sequence 3391 AA;

Query Match 100.0%; Score 53; DB 2; Length 3391;

Best Local Similarity 100.0%; Pred. No. 5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IETWILRHP 9
|||||

DB 237 IETWILRHP 245

Search completed: January 30, 2006, 09:13:02
Job time : 137 secs